```
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
```

- nucleic search, using sw model OM nucleic

Run on:

January 10, 2006, 19:25:44 ; Search time 328 Seconds (without alignments) 93.356 Million cell updates/sec

US-10-645-818-5 42 Title: Perfect score:

1 gagcttgggaagctcgtgct.....accaactgagctaccaccgc 42 Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

4637633 segs, 364532575 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA New:\*

1: /cgn2\_6/ptodata/1/pubpna/US06\_NEW PUB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW PUB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/US10\_NEW PUB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US11\_NEW PUB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US11\_NEW PUB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW PUB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW PUB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US10\_NEW PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Appl	Appli	Appl	Appl	Appl	31677, A	31677, A	51288, A	1288, A	45201, A	45201, A	30822, A	30822, A	79, Ap	38017, A	38017, A		2981, Ap		28416, A		77, Ap	
Ę	61	'n	24	10	30			51,	513	45	-		308	7779,			2981,	29	287	284	4402,	3707,	4217
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-11-075-185-61	US-11-088-257-1	US-10-933-025-24	US-11-088-257-10	US-11-088-257-30	US-10-750-185-31677	US-10-750-623-31677	US-10-750-185-51288	US-10-750-623-51288	US-10-750-185-45201	US-10-750-623-45201	US-10-750-185-30822	US-10-750-623-30822	US-10-467-657-7779	US-10-750-185-38017	US-10-750-623-38017	US-10-750-185-2981	US-10-750-623-2981	US-10-750-185-28416	US-10-750-623-28416	US-10-793-626-4402	US-10-793-626-3707	US-10-793-626-4217
8	7	7	9	7	7	ø	ø	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	ø
Length DB	4524	75	171936	25	25	5071	5071	1155	1155	1717	1717	2652	2652	216	2005	2005	598	598	1972	1972	2869	3012	3232
Query Match	100.0	74.8	57.1	55.7	55.7	54.8	54.8	54.3	54.3	53.8	53.8	53.8	53.8	53.3	52.4	52.4	51.9	51.9	51.9	51.9	51.9	51.9	51.9
Score	42	31.4	24	23.4	23.4	23	23	22.8	22.8	22.6	22.6	22.6	22.6	22.4	22	22	21.8	21.8	21.8	21.8	21.8	21.8	21.8
٠. بد	н	~	m	4	ß	9	7	80	6	0	٦.	Ŋ	m	4	Ŋ	ب	7	18	6	0	_	2	Ω.
Result No.		υ				υ	ပ			_	-	-	-	_	-	_	-	_	-	. 4	. 4		••

9	4	4	٩	٩	Å.	Q	æ	4	4	4	Þ	4	K	ø	Þ	4	Ø	K	Ø	4	4
4156. /	61996,	61996,	3435, 7		3435, 7	4245, 1	28606,	28606,	32066,	32066,	44624,	44624,	46898,	46898,	32953,	32953,	31644,	31644,	49010,	49010,	43967,
Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-10-793-626-4156	US-10-750-185-61996	-10-750-623-61996	US-10-750-185-3435	US-10-750-185-4245	US-10-750-623-3435	US-10-750-623-4245	US-10-750-185-28606	US-10-750-623-28606	JS-10-750-185-32066	JS-10-750-623-32066	JS-10-750-185-44624	US-10-750-623-44624	JS-10-750-185-46898	US-10-750-623-46898	JS-10-750-185-32953	US-10-750-623-32953	US-10-750-185-31644	JS-10-750-623-31644	JS-10-750-185-49010	JS-10-750-623-49010	JS-10-750-185-43967
G G	ë 9	Sn 9	n 9	9 0	9	n 9	_	_	0. 9	ă 9	G G		_	ñ 9	_	_	ğ 9	_	_	_	9
3305	598	598	009	900	009	009	910	910	972	972	1028	1028	1045	1045	1182	1182	1212	1212	1394	1394	1516
51.9	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4
21.8	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6
24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

```
Gaps
            Sequence 61, Application US/11075185

Publication No. US20050266434A1

GENERAL INFORMATION:

APPLICANT: REEVES, CRRISTOPHER D

APPLICANT: AULIEN, BRYAN

APPLICANT: AULIEN, BRYAN

APPLICANT: AULIEN, BRYAN

APPLICANT: AULIEN, BRYAN

TITLE OF INVENTION: BLOSYTHETIC GENE CLUSTER FOR AMBRUTICINS
FILE REFERENCE: 010099.03

CURRENT APPLICATION NUMBER: US/11/075,185

CURRENT APPLICATION NUMBER: US 60/551,103

PRIOR PILING DATE: 2004-03-08

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 42; DB 7; Length 4:
100.0%; Pred. No. 9.1e-08;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGCITGGGAAGCICGTGTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 61
LENGTH: 4524
US-11-075-185-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-075-185-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

3830 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 3871

ö

Sequence 1, Application US/11088257
Publication No. US20050260536A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Methods for Detection of Biological Organisms Using tRNA FILE OF INVENTION: Methods for Detection of Biological Organisms Using tRNA FILE OF INVENTION WUMBER: US/11/088,257
CURRENT APPLICATION NUMBER: US 60/555,683
FRIOR PILING DATE: 2004-03-24
NUMBER OF SEQ ID NOS: 30 US-11-088-257-1/c RESULT 2

2

```
) OTHER INFORMATION: Primer for bacteria US-11-088-257-30
; OTHER INFORMATION: Primer for bacteria
US-11-088-257-10
                                                                                                                                                        10 AAGCTCGTGCTCTACCAACTGAGCT 34
                                                                                                                                                                                               1 AAGGTCGTGCTCTACCAACTGAGCT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AAGCTCGTGCTCTACCAACTGAGCT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGGTCGTCTCTACCAACTGAGCT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31677, Application US/10750185 Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                      US-11-088-257-30
; Sequence 30, Application US/11088257
; Publication No. US20050260636A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Bovine 19866880454815
US-10-750-185-31677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 31677
LENGTH: 5071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
SEQ ID NO 30
LENGTH: 25
                                                                  Query Match 55.7%;
Best Local Similarity 96.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-750-185-31677/c
                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-11-088-257-10
| Sequence 10. Application US/11088257
| Sequence 10. Application US/11088257
| Sequence 10. Application NG 120050260636A1
| GENERAL INFORMATION:
| APPLICAMY: CELLEX INC
| TILLE OF INVENTION: Methods for Detection of Biological Organisms Using tRNA
| FILE REFERENCE: CELLEX--0006
| CURRENT TILING DATE: 2005-03-24
| PRIOR APPLICATION NUMBER: US 60/555,683
| PRIOR FILING DATE: 2004-03-24
| NUMBER OF SEQ ID NOS: 30
| SEQ ID NO 10
| LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 6; Length 171936;
Pred. No. 3.4;
0; Mismatches 10; Indels 0.
                                                                                                                                                                                                 Score 31.4; DB 7; Length 75; Pred. No. 0.00091; 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37347 écresceresécrescerriraceaecreadecaecaecaes 37386
                                                                                                                                                                                                                                                                                          1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCG 41
                                                                                                                                                                                                                                                                                                                      41 GACCTTGGCAGGTCGTGCTCTACCAACTGAGCTATTCCCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HEMMERICH, STEFAN
APPLICANT: TOMITA, MEGUMI
TITLE OF INVENTION: Sulfotransferases and methods of
TITLE OF INVENTION: thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: thereof
FILE REFERENCE: UCAL-230CON
CURRENT APPLICATION NUMBER: US/10/933,025
CURRENT FILING DATE: 2004-09-01
PRIOR PILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/256,577
PRIOR FILING DATE: 2001-09-02
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
                                                                                                                                 ; OTHER INFORMATION: Primer for bacteria US-11-088-257-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequenge 24, Application US/10933025
Publication No. US20050265987A1
APPLICANT: ROSEN, STEVEN
                                                                                                                                                                                                      74.8%;
85.4%;
    SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.1%;
Best Local Similarity 75.0%;
Matches 30; Conservative
                                                                                                                                                                                                                        Best Local Similarity 85.4
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus US-10-933-025-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: artificial FEATURE:
                                                                      TYPE: DNA
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171936
                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-933-025-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                    Query Match
                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
APPLICANT: CELLEX INC
TITLE OF INVENTION: Methods for Detection of Biological Organisms Using tRNA
TITLE REPERENCE: CELLEX--0006
CURRENT APPLICATION NUMBER: US/11/088,257
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: US 60/555,683
PRIOR FILING DATE: 2004-03-24
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: DENISE, Sue K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: RATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILLO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.8%; Score 23; DB 6; Length 5071; Best Local Similarity 74.4%; Pred. No. 4.7; Matches 29; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.7%; Score 23.4; DB 7; Length 25; Best Local Similarity 96.0%; Pred. No. 1.3; Matches 24; Conservative 0; Mismatches 1; Indels
  Length 25;
                                              1; Indels
7,
  DΒ
Score 23.4; Di
Pred. No. 1.3;
0; Mismatches
```

```
; TYPE: DNA
; ORGANISM: Bovine 19866880733794
US-10-750-623-51288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Bovine 19866881206092
US-10-750-185-45201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 45201
LENGTH: 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                APPLICANT: MINICANTION:
APPLICANT: DENISE, Sue K.
APPLICANT: ERRY, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: SAPILATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN Version 3.1
LENGTH: 5071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22.8; DB 6; Length 1155; Pred. No. 4.5; 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.8%; Score 23; DB 6; Length 5071; Best Local Similarity 74.4%; Pred. No. 4.7; Matches 29; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVERTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: WMILI100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1037 GAGCATCTCAAGCTCGTGCTCTGCAACAAGAAAACCACTGC 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                 1391 GCATTGCAAGCGGATTCTTACCAACTGAGCTATCACAG 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1391 GCATTGCAAGCGGATTCTTTACCAACTGAGCTATCACAG 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCG 41
                                                                                                                                                                           Sequence 31677, Application US/10750623
Publication No. US20050287531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51288, Application US/10750185
Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bovine 19866880454815
US-10-750-623-31677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Bovine 19866880733794
US-10-750-185-51288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 64922
SOFWARE: Patentin version 3.1
SEQ ID NO 51288
LENGTH: 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: WAI GENOMICS, INC.
APPLICANT: DenISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.4'
Matches 30; Conservative
                                                                                                                                                                                                                                  GENERAL INFORMATION
                                           g
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
```

A STATE TO A STATE OF THE

:

```
APPLICANT: KERR, Richard
APPLICANT: ROSENPELD, David
APPLICANT: ROSENPELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM: Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, STEPHEN
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SOFTWARE: LENGTH: 2652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.8%; Score 22.6; DB 6; Length 2652; Best Local Similarity 75.7%; Pred. No. 6.2; Matches 28; Conservative 0; Mismatches 9; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.3%; Score 22.4; DB 6; Length 216; Best Local Similarity 72.5%; Pred. No. 4.9; Matches 29; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7779, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNAIN Vega
APPLICANT: MASIGNAIN Vega
APPLICANT: MASIGNAIN VEGA
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLBIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 écaréccarecaaécecreraceaacreaécraracecee 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1319 TIGGCAGGTGGGTTCTCTACCACCTGAGCCACCACGG 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TIGGGAAGCICGIGCICTACCAACIGAGCIACCACCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin59, version 1.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 38017, Application US/10750185
Publication No. US2050260603A1
Publication No. US2050260603A1
APPLICANT: WMI GENOMICS, INC.
APPLICANT: DeNISB, SUB K.
APPLICANT: RERK, Richard
APPLICANT: RERK, Richard
APPLICANT: ROSENPELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Bovine 19866880468477
US-10-750-623-30822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7779
                                                        DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-750-185-38017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-10-467-657-7779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Sequence 45201.
Sequence 45201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-750-185-30822

US-10-750-185-30822

Sequence 3 0822, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:
APPLICANT: WMI GENOWICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
ITILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: WMINIOG-2
CURRENT FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 30822
HANDEL OF SEQ ID NOS: 64922
SEQ ID NO 30822
HANDEL OF SEQ ID NOS: 64922
SEQ ID NO 30822
HANDEL OF SEQ ID NOS: 64922
SEQ ID NO 30822
HANDEL OF SEQ ID NOS: 64922
SEQ ID NO 30822
HANDEL OF SEQ ID NOS: 64922
SEQ ID NO 30822
SEQ ID NO 30822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 2652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1319 TTGGCAGGTGGGTTCTCTACCACCTGAGCCACCACGG 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1601 Tregcaegeracircirraccaecreaeccaecae 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 TTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 TIGGGAAGCICGIGCICIACCAACIGAGCIACCACCG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22.6; DB 6;
Pred. No. 5.7;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22.6; D
Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
0-10-750-623-30822
; Sequence 30822, Application US/10750623
; Publication No. US20050287531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bovine 19866881206092
US-10-750-623-45201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Bovine 19866880468477
US-10-750-185-30822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 53.8%;
1 Similarity 75.7%;
28; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.8%;
Best Local Similarity 75.7%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
```

ઠે 셤 ö

Gaps

ö

42

ò 엄

ö

Gaps

```
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILION-2
CURRENT FILING DATE: 2003-12-31
FRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 38017
LENGTH: 2005
TYPE: DAB
ORGANISM: Bovine 19866880521244
US-10-750-185-38017
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.4%; Score 22; DB 6; Length 2005; Best Local Similarity 73.7%; Pred. No. 10; Matches 28; Conservative 0; Mismatches 10; Indels
```

579 GCATTGCAGGCTGATTCTTTACCAACTGAGCTATCAGC 616 3 GCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACC 40 ò g

Search completed: January 10, 2006, 21:48:32 Job time : 329 secs

(olden) Missifa Books Hill

Н

us-10-645-818-5.rni

```
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
```

- nucleic search, using sw model OM nucleic

Run on:

January 10, 2006, 17:18:09; Search time 140 Seconds (without alignments) 533.268 Million cell updates/sec

US-10-645-818-5 42

Perfect score:

1 gagettgggaagetegtget........accaactgagetaccacege 42 Scoring table: Seguence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

2606114 Total number of hits satisfying chosen parameters:

1303057 seqs, 888780828 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued Patents NA:\*

1: /cgn2 6/ptodata1/ina/1\_COMB.seq:\*

2: /cgn2 6/ptodata1/ina/5\_COMB.seq:\*

3: /cgn2 6/ptodata1/ina/6A\_COMB.seq:\*

4: /cgn2 6/ptodata1/ina/6B\_COMB.seq:\*

5: /cgn2 6/ptodata1/ina/H\_COMB.seq:\*

6: /cgn2 6/ptodata1/ina/H\_COMB.seq:\*

7: /cgn2 6/ptodata1/ina/PE\_COMB.seq:\*

8: /cgn2 6/ptodata1/ina/PE\_COMB.seq:\*

9: /cgn2 6/ptodata1/ina/RE\_COMB.seq:\*

9: /cgn2 6/ptodata1/ina/RE\_COMB.seq:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Sequence 657, App	Sequence 104, App	٠.	Sequence 15110, A	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	'n	Sequence 1, Appli	Sequence 1, Appli	25,	Sequence 33, Appl	1,	Sequence 1, Appli	Sequence 1, Appli	Sequence 3919, Ap	Sequence 650, App	Sequence 1090, Ap		Sequence 726, App	878,	Sequence 85, Appl	Sequence 86, Appl
	QI	US-09-902-540-657	US-09-540-236-104	US-09-252-991A-14851	US-09-252-991A-15110	US-08-287-442-3	US-08-459-701-3	US-08-460-298-3	US-08-459-174-3	PCT-US93-06300A-3	US-08-761-258-1	US-08-977-306-1	US-09-596-002-25	US-09-596-002-33	US-09-557-884-1	US-09-643-990A-1	US-10-158-865-1	US-09-543-681A-3919	US-09-221-017B-650	US-09-221-017B-1090	US-09-790-988-1	US-09-328-352-726	US-09-902-540-878	US-08-412-614-85	US-08-412-614-86
	DB	3	m	m	m	7	7	7	0	9	~	~	m	m	e	m	m	m	m	m	٣	m	m	7	~
	Query Match Length DB	4575	258	549	069	5559	5559	5559	5559	5559	10763	10763	31147	63563	1830121	1830121	1830121	339	5595	18431	640681	282	7035	603	603
de	Query Match	100.0	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	71.0	71.0	71.0	71.0	67.1	67.1	64.8	64.8
	Score	42	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	29.8	29.8	29.8	29.8	28.2	28.2	27.2	27.2
	Result No.	7	~	3	4	S	9	7	80	6	10	11	c 12	c 13	c 14	c 15	c 16	17	18	c 19	c 50	21	22	c 23	c 24

86,7	Sequence 85, Appl Sequence 89, Appl Sequence 89, Appl Sequence 89, Appl Sequence 89, Appl Sequence 926, App	Sequence 2, Appli Sequence 1, Appli Sequence 17468, A Sequence 131, App Sequence 132, App	Sequence 131, App Sequence 132, App Sequence 131, App Sequence 132, App Sequence 154, App
US-08-635-761-85 US-08-635-761-86 US-09-312-520-85 US-09-312-520-86 US-09-312-520-86	US-09-618-86 US-08-635-761-89 US-09-312-520-89 US-09-863-086-89 US-08-412-614-89 US-09-902-540-926	US-09-103-840A-2 US-09-103-840A-1 US-09-949-016-17468 US-08-765-332-131 US-08-765-332-132	US-09-448-894-131 US-09-448-894-132 US-09-931-486-131 US-09-931-486-132 US-08-765-332-154
0.00000		 	<b>мммм</b>
00000000000000000000000000000000000000	6554 6554 6554 5993	4403765 4411529 88906 808 808	808 808 808 808
	64.8 64.8 64.8 63.8 63.8	63.3 63.3 61.4 61.0	61.0 61.0 61.0 61.0
444444	4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	63.3 61.4 61.0 61.0	66666
22.722	22.72 24.72 24.72 26.72 26.63	26.6 25.8 25.8 25.6	25.6 25.6 25.6 25.6 25.6
2222	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 8 8 8 4 9 8 8 9 9	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
00000	0 0 0 0 0	00 00	00000

#### ALIGNMENTS

```
ö
          Sequence 657, Application US/09902540

Patent No. 683347

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
CURRENT FILE REFERENCE: 38-10(15849)B
CURRENT FILE O DATE: 2001-07-10
PRIOR PILICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1981 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGCTTGGGAAGCTCGTGTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 42; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 42; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; ORGANISM: Myxococcus xanthus US-09-902-540-657
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 657
US-09-902-540-657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
```

```
Sequence 104, Application US/09540236

Batent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NOS: 3840
SEQ ID NO 104
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: M.catarrhalis
RESULT 2
US-09-540-236-104
```

ò В

```
NAME/KEY: misc_feature
LOCATION: 1906..3633
OTHER INFORMATION: /note= "ORF 2, transcribed left to
OTHER INFORMATION: right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 210..1688
OTHER INFORMATION: /note= "ORF 1, transcribed left to
OTHER INFORMATION: right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.6 kb EcoRI-HindIII restriction fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                      Gene Activating Element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,636
FILING DATE: 01-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,284
FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/570,184
FILING DATE: 08-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: BIMER: JURGES SOCIET
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GGC 1506/CIP4
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, N
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                          Sequence 3, Application US/08287442
Patent No. 5670350
GENERAL INFORMATION:
                                                                                                             APPLICANT: Gaffney, Thomas D. APPLICANT: Lam, Stephen T. APPLICANT: Ligon, James M. APPLICANT: Hill, Dwight S. APPLICANT: Hill, Dwight S. APPLICANT: Stein, Jeffrey I. APPLICANT: Becker, J. Ole TITLE OF INVENTION: Gene Activa NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5559 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE: 5
INDIVIDUAL ISOLATE: 5
INMEDIATE SOURCE:
CLONE: pCIBL37
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10532
                        US-08-287-442-3
                                                                                                                                                                                                                                                                                           Sequence 1916. Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 14851

LENGTH: 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANTION:
APPLICANT:
AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15100
LENGTH: 690
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                              ö
                                            Score 32.4; DB 3; Length 258;
Pred. No. 0.0019;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32.4; DB 3; Length 549;
Pred. No. 0.0022;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 77.1%; Score 32.4; DB 3; Length 690; Best Local Similarity 85.7%; Pred. No. 0.0023; Matches 36; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 GACCTIGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 519
                                                                                                                                                                                        113 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15110, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15110
                                            77.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.7
Matches 36, Conservative
                                                                   Local Similarity 85.7
hes 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-252-991A-15110
                                                                                                                                                                                                                                                                                    US-09-252-991A-14851
US-09-540-236-104
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

à a ద

ð

```
ANTI-SERNE:
ORGANISM: Bounce:
ORGANISM: Peeudomonas fluorescens
STRAIN: CGA267356
INDIVIDUAL ISOLATE: 5.6 kb ECORI-HindIII restriction
INDIVIDUAL ISOLATE: fragment
INFORMATION: /note= "ORF 1, transcribed left to
OTHER INFORMATION: /note= "ORF 2, transcribed left to
OTHER INFORMATION: /note= "ORF 2, transcribed right to
OTHER INFORMATION: /note= "Glyw, transcribed right to
OTHER INFORMATION: /note= "Glyw, transcribed right to
OTHER INFORMATION: /note= "Glyw, transcribed right to
OTHER INFORMATION: /note= "ORF 3, transcribed right to
OTHER INFORMATION: left"
FRATURE:
NAME/KEY: misc_feature
LOCATION: A131..5318
INFORMATION: left"
OTHER INFORMATION: left"
COTHER INFORMATION: left"
US-08-459-701-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 77.1%; Score 32.4; DB 2; Length 5559; Best Local Similarity 85.7%; Pred. No. 0.0037; Matches 36; Conservative 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4650 GACCTIGGCAAGGICGIGCICIACCAACTGAGCIATICCCGC 4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BATENIN PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SUFFWARE: PATENIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/460,298
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gaffney, Thomas D.
APPLICANT: Lam, Stephen T.
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Hill, Dwight S.
APPLICANT: Howell, Charles R.
APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
ITLE OF INVENTION: Gene Activating Element
NUMBER OF SEQUENCES: 9
CORRESPENDENCES: ADDRESSE: ADDRESSE: TEA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STREET: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08460298
Patent No. 5686283
                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
           linear
                                                                                            ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-460-298-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                   Query Match 77.1%; Score 32.4; DB 2; Length 5559; Best Local Similarity 85.7%; Pred. No. 0.0037; Matches 36; Conservative 0; Mismatches 6; Indels 0
NAME/KEY: misc_feature

COCATION: 4616_.4691

OTHER INFORMATION: /note= "glyW, transcribed right to other information: left"
FRATURE:
NAME/KEY: misc_feature
COCHER INFORMATION: /note= "ORF 3, transcribed right to other information: left"
OTHER INFORMATION: /note= "ORF 3, transcribed right to us-ob-287-442-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4650 cacciricacaacciccicriciaccaacicaaciairreccec 4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CUASSIFICATION NUMBER: US/08/459,701
FILING DATE: 02-UUN-1995
FILING DATE: 08-AUG-1994
APPLICATION NUMBER: US 08/287,442
APPLICATION NUMBER: US 08/087,636
FILING DATE: 01-ULL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,284
FILING DATE: 02-ULL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/570,184
FILING DATE: US 08-UG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GG 1506/CIP4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gaffney, Thomas D.
APPLICANT: Lam, Stephen T.
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TILLE OF INVENTION: Gene Activating Element
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: CIBA-GEIGY Corporation
7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08459701
Patent No. 5686282
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 5559 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-459-701-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

Gaps

```
NAME/KEY: misc_feature
LOCATION: 210..1688
OTHER INPORMATION: /note= "ORF 1, transcribed left to
OTHER INFORMATION: right"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1906..3633
OTHER INFORMATION: right"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4016..4691
OTHER INFORMATION: /note= "glyW, transcribed right to
OTHER INFORMATION: /note= "glyW, transcribed right to
DOTHER INFORMATION: /note= "glyW, transcribed right to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.6 kb EcoRI-HindIII restriction fragment
                                                                                                                                                                                                                                                                                     COMPUTER: USAA
ZIP: 10532
COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,174
FILING DATE: 02-UNA-1995
CLASSIFICATION STAF
FILING DATE: 01-UL-1993
PRIOR APPLICATION NUMBER: US 08/287,442
FILING DATE: 01-UL-1993
PRIOR APPLICATION NUMBER: US 07/908,284
FILING DATE: 01-UL-1993
PRIOR APPLICATION NUMBER: US 07/570,184
FILING DATE: 08-AUG-1990
APPLICATION NUMBER: US 07/570,184
FILING DATE: 08-AUG-1990
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 36,129
FRIOR APPLICATION NUMBER: 36,129
FRIOR APPLICATION NUMBER: 36,129
FRIEFRAN: 919-541-869
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5559 base pairs
TTELEPANDENESS: single
TODOLOGY: 11near
                      APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TITLE OF INVENTION: Gene Activating Element
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STRTE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356
INDIVIDUAL ISOLATE: 5.6 kb ECORI-Hin
INDIVIDUAL ISOLATE: fragment
INMEDIATE SOURCE:
CLONE: PCIBL37
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature 4731..5318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.1%; Score 32.4; DB 2; Length 5559; Best Local Similarity 85.7%; Pred. No. 0.0037; Matches 36; Conservative 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 4731.5318
OTHER INFORMATION: /note= "ORF 3, transcribed right to
OTHER INFORMATION: left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 1906...363
OTHER INFORMATION: '/note= "ORF 2, transcribed left to
OTHER INFORMATION: right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: 210._1688
OTHER INFORMATION: /note= "ORF 1, transcribed left to
OTHER INFORMATION: right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4650 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.6 kb EcoRI-HindIII restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 4616.4691
CHER INFORMATION: //note= "glyW, transcribed right
OTHER INFORMATION: //note= //other information: left"
APPLICATION NUMBER: US USUS, CONTROLLE OF THIME DATE: 08-AUG-1994
APPLICATION NUMBER: US 08/087,636
FILING DATE: 01-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,284
FILING DATE: 02-JUL-1992
PRIOR APPLICATION NUMBER: US 07/570,184
FILING DATE: 08-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bimer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GG 1506/CIP4
TELEPHONE: 919-541-6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356
INDIVIDUAL ISOLATE: 5.6 kb ECORI-F
INDIVIDUAL ISOLATE: fragment
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-459-174-3
; Sequence 3, Application US/08459174
; Patent No. 5710031
; GENERAL INFORMATION:
; APPLICANT: Lam, Stephen T.
; APPLICANT: Ligon, James M.
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-460-298-3
```

RESULT 8

ò

ហ

셤 ò

```
GENERAL INFORMATION:

APPLICANT: Ligon, James M.
APPLICANT: Ligon, James M.
APPLICANT: Lam, Stephen T.
APPLICANT: Lam, Stephen T.
APPLICANT: Gaffney, Thomas D.
APPLICANT: Torkewitz, Nancy
TITLE OF INVENTION: Genetically Modified Pseudomonas Strains
TITLE OF INVENTION: with Enhanced Biocontrol Activity
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCES: Ciba-Geigy Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 77.1%; Score 32.4; DB 6; Length 5559; Best Local Similarity 85.7%; Pred. No. 0.0037; Matches 36; Conservative 0; Mismatches 6; Indels 0
TELEFAX: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH = S559 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens
STRAIN: Pseudomonas fluorescens
STRAIN: CGAZGY356
INDIVIDUAL ISOLATE: 5.6 kb ECORI-HindIII restriction
INDIVIDUAL ISOLATE: fragment
INDIVIDUAL SOURCE:
CLONE: PCIB137
FEATURE:
NAME/KEY: misc feature
LOCATION: 210..1688
OTHER INFORMATION: /note= "ORF 1, transcribed left to
OTHER INFORMATION: right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KRY: misc feature
; LOCATION: 4731_.5318
; OTHER INFORMATION: /note= "ORF 3, transcribed right to
; OTHER INFORMATION: left"
PCT-US93-06300A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 4616..4691
OTHER INFORMATION: /note= "glyW, transcribed right to
OTHER INFORMATION: left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1906..363
OCHER INFORMATION: /note= "ORF 2, transcribed left to
OTHER INFORMATION: right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4650 GACCTIGGCAAGGICGIGCICIACCAACIGAGCIATICCCGC 4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08761258
Patent No. 5756087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-761-258-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                            ö
                                                                                                                                            Gaps
                                                                                                                                            ö
                                                                                              Query Match 77.1%; Score 32.4; DB 2; Length 5559; Best Local Similarity 85.7%; Pred. No. 0.0037; Matches 36; Conservative 0; Mismatches 6; Indels 0
               /note= "ORF 3, transcribed right to
left"
                                                                                                                                                                                                                         4650 GACCTIGGCAAGGICGIGCTCIACCAACTGAGCTATICCCGC 4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06300A
FILING DATE: 02-JUL-1993
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 07/908,284
FILING DATE: 02-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MULTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18210/A/CGC1506/PC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Gene Activating Element NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8: CIBA-GEIGY Corporation 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                        Sequence 3, Application PC/TUS9306300A
GENERAL INFORMATION:
APPLICANT: CIRA-GEIGY AG
APPLICANT: Klybeckstrasse 141
APPLICANT: 4002 Basle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stein, Jeffrey I.
3725 Surry Trail
Hillsborough, NC 27278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 Tradescant Road
Chapel Hill, NC 27514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6164 Osevego
Riverside, CA 92506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hill, Dwight Steven
311 Melanie Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligon, James M.
120 Marquette Drive
Cary, NC 27513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8900 Jeanew Court
Raleigh, NC 27613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Howell, Charles R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               805 Avondale
Bryan, TX 77802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cary, NC 27511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Becker, J. Ole
                                                                                                                                                                                                                                                                                                                                                                                                                                          Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIG
STREET: 7 Skyline Dr.
             ) OTHER INFORMATION:

) OTHER INFORMATION:

US-08-459-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                               PCT-US93-06300A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT
```

ö

Gaps

```
/note= "Coding sequence for methyltransferase has homology to the cheR and fizz genes from E. coli and Myxococcus xanthus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1966-3633
OTHER INFORMATION: /product= "sensor kinase"
OTHER INFORMATION: /note= "coding sequence for sensor kinase has homology to the OTHER INFORMATION: rcsC, frzE, and byeg genes of E. coli, M. Xanthus, and OTHER INFORMATION: Borditella pertussis, respectively."
                                          ö
                                          Gaps
                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Gaffney, Thomas D.
APPLICANT: Stafford, Jill M.
APPLICANT: Stafford, Jill M.
APPLICANT: Stafford, Jill M.
APPLICANT: Stafford, Jill M.
APPLICANT: Wancy
APPLICANT: Wancy
APPLICANT: Stafford, Jill M.
APPLICANT: M.
APPLICANT
                                          6; Indels
                                                                                                                                                                                   4650 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCCGC 4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KRY: misc_feature
LOCATION: 210._1688
LOCATION: /product= "methyltransferase"
OTHER INFORMATION: /note="Coding sequence for me
OTHER INFORMATION: the cheR and frzf genes from E
OTHER INFORMATION: respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356 (aka MOCG134 and aka BL915)
Best Local Similarity 85.7%; Pred. No. 0.0043; Matches 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 5955348artis Corporation
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08977306
Patent No. 5955348
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INPORMATION:
NAME: Meigs. U. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPAX: (919) 541-869
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10763 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1906..3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: Plasmid pE11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                         US-08-977-306-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EATURE:
                                                                                                                  8
                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 210..1688
OTHER INFORMATION: /product= "methyltransferase"
OTHER INFORMATION: /product= "Coding sequence for methyltransferase has homology to OTHER INFORMATION: the cheR and frzF genes from E. coli and Myxococcus xanthus, OTHER INFORMATION: respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "sensor kinase"
fnote= "Coding sequence for sensor kinase has homology to the
rcsc, frzE, and byeS genes of E. coli, M. Xanthus, and
Borditella pertussis, respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atidyltrans."
/note= "Coding sequence for
CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltransfe
se has homology to pgsA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMATION: function= "response
RMATION: regulator/transcription activator"
RMATION: /product= "gacA (aka gafA)"
RMATION: /product= "cding sequence for gacA (aka gafA) has homology to
RMATION: uvrY and gacA genes of E. coli and Ps. fluorescens,
RMATION: respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_RNA
LOCATION: complement (4616..4691)
OTHER INFORMATION: /product= "tRNA"
OTHER INFORMATION: /note= "(complementary DNA strand) Homology to glyW from E.
OTHER INFORMATION: Coli."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Coding sequence for UVR exonuclease subunit C has homology to uvrC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product=
"CDP-diacylglycerol-glycerol-3-phosphate-3-phosph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: complement (5574..7397)
OTHER INFORMATION: /product= "UVR exonuclease subunit
OTHER INFORMATION:
C"
OTHER INFORMATION:
Anote= "Coding sequence for UVR exc
OTHER INFORMATION: /note= "Coding sequence for UVR exc
   SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356 (aka MOCG134 and aka BL915)
IMMBILATE SOURCE:
CLONE: Plasmid pE11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc feature
'^^ation: complement (4731..5318)
'^^ation: hyroduct=
                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,258
                                                                                                                                                                            ATTORNEY/ACENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: PBeudomonas fluore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 1906..3633
OTHER INFORMATION: /prod
OTHER INFORMATION: /note
OTHER INFORMATION: csc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: complement (74
OTHER INFORMATION: /func
OTHER INFORMATION: regul
OTHER INFORMATION: /prode
                                                                                                           FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: complement
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-761-258-1
```

NAME/KEY: misc RNA

77.1%; Score 32.4; DB 2; Length 10763;

Query Match

complement (4616..4691)

```
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME FILE REFERENCE: PM-0008-4 US
FILE REFERENCE: PM-0008-4 US
CURRENT PEPLING DATE: 08/09/596,002
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fleischmann et al. TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.1%; Score 32.4; DB 3; Length 63563; 85.7%; Pred. No. 0.0064; tive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1051 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
) OTHER INFORMATION: Incyte template ID No. 6632636 33
; PUBLICATION INFORMATION:
US-09-596-002-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,911
REFERENCE/DOCKET NUMBER: PB186F93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                    Sequence 33, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
APPLICANT: Lagace, Robert, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                   Lagace, Robert, E.
Patterson, Chandra
Berg, Kim, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09557884 Patent No. 6506581 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS ADDRESSE: Human (
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 85.7
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                              US-09-596-002-33/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 33
LENGTH: 63563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-557-884-1/c
                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                              /note= "Coding sequence for
CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltransfe
se has homology to pgsA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nt (7400..8041)
/function= "response
regulator/transcription activator"
/product= "gacA (aka gafA)"
/note= "Coding sequence for gacA (aka gafA) has homology to uvrY and gacA genes of E. coli and Ps. fluorescens, respectively."
                           /product= "tRNA"
/note= "(complementary DNA strand) Homology to glyW from E.
Coli."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Coding sequence for UVR exonuclease subunit C has homology to uvrC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lagace, Robert, E. APPLICANT: Lagace, Robert, E. APPLICANT: Patterson, Chandra APPLICANT: Patterson, Chandra APPLICANT: BELY Kim, L. 11TLE OF INVENTION: UNCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME FILE REPERBANCE: PM-0008-4 US CURRENT APPLICATION NUMBER: US/09/596,002 CURRENT FILING DATE: 2000-06-16 PRIOR APPLICATION NUMBER: 60/140,121 PRIOR PILING DATE: 1999-06-18 NUMBER: OF SEQ ID NOS: 41 SOFTWARE: PERL PROGram
                                                                                                                          NAME/KEY: misc_feature
LOCATION: complement (4731..5318)
COTHER INFORMATION: "CDP-duct=-07HBZ
OTHER INFORMATION: "CDP-diacylglycerol-glycerol-3-phosphate-3-phosph
OTHER INFORMATION: "Ance="Coding sequence for OTHER INFORMATION: "CDP-diacylglycerol-glycerol-3-phosphate-3-phosphate INFORMATION: CBP-diacylglycerol-glycerol-3-phosphate-3-phosphate OTHER INFORMATION: se has homology to pgsA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.1%; Score 32.4; DB 2; Length 10763; Best Local Similarity 85.7%; Pred. No. 0.0043; Matches 36; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32.4; DB 3; Length 31147;
Pred. No. 0.0054;
0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13927 GACCTTGCCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 13886
                                                                                                                                                                                                                                                                                                                                                                                                   /product= "UVR exonuclease subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4650 GACCITGGCAAGGICGIGCICTACCAACIGAGCIATICCCGC 4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte template ID No. 6632636 25
; PUBLICATION INFORMATION:
US-09-596-002-25
                                                                                                                                                                                                                                                                                                                                                                                              (5574..7397)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
APPLICAINT: Lagace, Robert, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 77.1%;
Best Local Similarity 85.7%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature LOCATION: complement (f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc feature
LOCATION: complement (7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: M. catarrhalis
LOCATION: complement
OTHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: C
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-596-002-25/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 25
LENGTH: 31147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-977-306-1
```

8

ò

と からあい

g

δ

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mark D. Adams
Mark D. Adams
Wann White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.1%; Score 32.4; DB 3; Length 1830121; Best Local Similarity 85.7%; Pred. No. 0.014; Matches 36; Conservative 0; Mismatches 6; Indels 0; (
                                                                                                                                                                                                   Query Match 77.1%; Score 32.4; DB 3; Length 1830121; Best Local Similarity 85.7%; Pred. No. 0.014; Aatches 36; Conservative 0; Mismatches 6; Indels 0; (
                                                                                                                                                                                                                                                                                                                      90995 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 90954
                                                                                                                                                                                                                                                                                       1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER FOLKANIA COMPUTER COMPUTER COMPUTER: Dell Pentium OPERATING SYSTEM: MS DOS V6.22 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000 CLASSIFICATION NUMBER: 08/42, PRIOR APPLICATION NUMBER: 08/42, 787 FILING DATE: 1995-06-07 APPLICATION NUMBER: 08/426,787 FILING DATE: 1995-04-21 ATTORNEY/AGENT INFORMATION: NAME: Kenley K. Hoover REGISTRATION NUMBER: 40,302 REFERENCE/DOCKET NUMBER: 40,302 TELEFARAISHICS: TELEFARAISHICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 1830121 base pairs TYRNE INCOLES COLD
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6238289
; GENERAL INFORMATION:
; APPLICANT: ROBERT D. Fleischmann
, APPLICANT: ROBERT D. APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-643-990A-1
                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                 셤
```

ö

Gaps

```
Search completed: January 10, 2006, 19:28:15
Job time : 150 secs
                 g
  ઠ
```

us-10-645-818-5 \rhpbm

```
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
```

- nucleic search, using sw model

OM nucleic

Run on:

January 10, 2006, 18:22:31; Search time 815 Seconds (without alignments) 426.152 Million cell updates/sec

US-10-645-818-5 42

Title: Perfect score:

1 gagettgggaagetegtget.....accaaetgagetaccaeege Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

9793542 segs, 4134689005 residues Searched:

19587084 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA Main:\*

1: /cgn2 6/ptodata/1/pubpna/USO3\_PUBCOMB.seq:\*
2: /cgn2\_6/ptodata/1/pubpna/USO3\_PUBCOMB.seq:\*
3: /cgn2\_6/ptodata/1/pubpna/USO3B\_PUBCOMB.seq:\*
4: /cgn2\_6/ptodata/1/pubpna/USO3B\_PUBCOMB.seq:\*
5: /cgn2\_6/ptodata/1/pubpna/USO3B\_PUBCOMB.seq:\*
6: /cgn2\_6/ptodata/1/pubpna/USO3B\_PUBCOMB.seq:\*
7: /cgn2\_6/ptodata/1/pubpna/USO3B\_PUBCOMB.seq:\*
8: /cgn2\_6/ptodata/1/pubpna/USO3D\_PUBCOMB.seq:\*
9: /cgn2\_6/ptodata/1/pubpna/USO3D\_PUBCOMB.seq:\*
9: /cgn2\_6/ptodata/1/pubpna/USO3D\_PUBCOMB.seq:\*
10: /cgn2\_6/ptodata/1/pubpna/USO3D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Sequence 5, Appli	Sequence 12, Appl	Sequence 7, Appli	'n	Sequence 4, Appli	Sequence 1, Appli	378	Sequence 201, App	Sequence 492, App	Sequence 575, App	Sequence 25, Appl	Sequence 33, Appl	Sequence 684, App	Sequence 685, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 650, App	Sequence 1090, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 14, Appl
ID	US-10-645-818-5	US-10-645-818-12	US-10-645-818-7	US-10-645-818-3	US-10-645-818-4	US-10-645-818-1	US-09-815-242-3781	US-10-795-159-201	US-10-795-159-492	US-10-795-159-575	US-10-672-787-25	US-10-672-787-33	US-10-795-159-684	US-10-795-159-685	US-10-329-670-1	US-10-158-865-1	US-10-981-687-1	US-10-194-163-650	US-10-194-163-1090	US-09-790-988-1	US-10-156-761-1	US-10-156-761-1	US-10-915-740A-14
80	8	ထ	œ	œ	8	8	٣	6	σ	σ	7	7	σ	σ	7	æ	σ	ß	ß	m	9	9	6
* Query Match Length DB	42	74	257	360	360	1647	657	1960	5436	28871	31147	63563	417576	908766	1830121	1830121	1830121	5595	18431	640681	9025608	9025608	4927
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	71.0	71.0	71.0	71.0	71.0	67.1
Score	42	42	42	42	42	42	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	29.8	29.8	29.8	29.8	29.8	28.2
Result No.		0	٣	4	'n	9	C 7	80	0	c 10	c 11	c 12	c 13	c 14	c 15	c 16	c 17	18	c 19	c 20	21	c 25	23

85, 85, 86, 86,	Sequence 89, Appl Sequence 8, Appli Sequence 1068, Ap Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	322 132 132 154 154
US-10-915-740A-1068 US-10-297-465A-1 US-09-863-086-85 US-09-863-086-86 US-10-672-238-85 US-10-672-238-86 US-09-863-086-89	US-10-672-238-89 US-10-915-740A-8 US-10-915-740A-1068 US-09-738-626-1 US-09-738-656-1 US-10-297-465A-1	US-10-655-847-4 US-10-717-597-322 US-09-931-486-133 US-09-931-486-133 US-10-895-114-133 US-10-895-114-132 US-10-9931-486-154 US-10-895-114-154
97 88778	ر م م م م ر	, r r m m o o m o
2242716 2731748 603 603 603 603 654	654 20844 2242716 3309400 3309400 2731748	1704245 170245 808 808 808 808 808 808
64.8 64.8 64.8 64.8 64.8 64.8	64.8 64.8 63.8 61.9	4.4.00.199.0
28.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27	27.2.2 26.2.2.2 26.6.2 26.6.2	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
30 8 8 7 8 8 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	32 32 32 32 32 32 32	26644444 44422 544324098
υυυυυ	υυυυ υ	0000000

### ALIGNMENTS

```
US-10-645-818-5

Sequence 5, Application US/10645818

Publication No. US20040247620A1

Sequence 5, Application US. US20040247620A1

GENERAL INFORMATION:

APPLICANT: Koan Biosciences, Inc.

APPLICANT: Koan Biosciences, Inc.

TITLE OF INVENTION: INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS

TITLE OF INVENTION: BACTERIOPHAGE MX9

FILE REFERENCE: 300622009940

CURRENT PILING DATE: 2003-08-20

CURRENT PILING DATE: 2003-08-20

PRIOR APPLICATION NUMBER: US 60/405,196

PRIOR APPLICATION NUMBER: 2003-08-21

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PSEUSEQ for Windows Version 4.0

SEG ID NO 5

LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGCTIGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 8; I
Pred. No. 3.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 42; DB
Best Local Similarity 100.0%; Pred. No. 3.4
Matches 42; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Bacteriophage MX9
US-10-645-818-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

US-10-645-818-12/c

셤

Sequence 12, Application US/10645818 Publication No. US20040247620A1 GENERAL INFORMATION:

APPLICANT: Kosan Biosciences, Inc. APPLICANT: Julien, Bryan

APPLICANT: JULIEN, Bryan
TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE
TITLE OF INVENTION: INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
TITLE OF INVENTION: BACTERIOPHAGE MX9
FILE REFERENCE: 300622009940

CURRENT APPLICATION NUMBER: US/10/645,818 CURRENT FILING DATE: 2003-08-20 PRIOR APPLICATION NUMBER: US 60/405,196

というないないとない

us-10-645-818-5.rnpbm

```
Query Match 100.
Best Local Similarity 100.
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1647
                                                                                                                                                                                                                                                      US-10-645-818-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-645-818-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-645-818-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                          ઠ
                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10645818
Publication No. US20040247620A1
GENERAL INFORMATION:
APPLICANT: Mosan Bloscience, Inc.
APPLICANT: Julien, Bryan
TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE
TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE
TITLE OF INVENTION: BACTERIOPHAGE MX9
TITLE OF INVENTION: BACTERIOPHAGE MX9
TITLE OF INVENTION: BACTERIOPHAGE WX9
CURRENT APPLICATION NUMBER: US/10/645,818
CURRENT APPLICATION NUMBER: US 60/405,196
PRIOR APPLICATION NUMBER: US 60/405,196
PRIOR PILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kosan Biosciences, Inc.
APPLICANT: Valien, Baysan
TITLE OF INVENTION: TRANSPORMATION SYSTEM BASED ON THE
TITLE OF INVENTION: INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
TITLE OF INVENTION: BACTERIOPHAGE MX9
FILE REFERENCE: 300622009940
CURRENT APPLICATION NUMBER: US/10/645,818
FRICH REPERENCE: 2003-08-20
FRICH REPLICATION NUMBER: US 60/405,196
FRICH REPLICATION DATE: 2002-08-21
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 42; DB 8; Length 257; Best Local Similarity 100.0%; Pred. No. 4.3e-07; Matches 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                        Query Match 100.0%; Score 42; DB 8; Length 74; Best Local Similarity 100.0%; Pred. No. 3.6e-07; Matches 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 156
                                                                                                                                                                                                                                                                                                                              1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                          42 GAGCTIGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 1
PRIOR FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10645818
Publication No. US20040247620A1
GENERAL INFORMATION:
                                                                                                                            TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Bacteriophage MX9
US-10-645-818-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Bacteriophage MX9
US-10-645-818-7
                                                                                                                                                                             US-10-645-818-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 7
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-645-818-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-645-818-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
APPLICANT: Kosan Biosciences, Inc.
APPLICANT: Volien, Bryan
APPLICANT: Julien, Bryan
TITLE OF INVENTION: TREERASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
TITLE OF INVENTION: BACTERIOPHAGE MX9
TITLE OF INVENTION: BACTERIOPHAGE MX9
TITLE OF INVENTION: BACTERIOPHAGE MX9
CURRENT APPLICATION NUMBER: US/10/645,818
CURRENT APPLICATION NUMBER: US 60/405,196
PRIOR FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 20
SOUTWARE: FASELSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kosan Biosciences, Inc.
APPLICANT: Julien, Bryan
TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE
TITLE OF INVENTION: INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
TITLE OF INVENTION: BACTERIOPHAGE MX9
FILE REFERENCE: 300622009940
FILE REFERENCE: 300622009940
CURRENT APPLICATION NUMBER: US, 10/645, 818
CURRENT FILING DATE: 2003-08-20
PRIOR FILING DATE: 2002-08-21
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 360;
     Length 360;
                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1394 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 206
                                                                                                                                                             163 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 204
                                                                                                                1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 42; DB 8; I
Best Local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 42; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 42; DB 8; 1
100.0%; Pred. No. 5.4e-07;
ive 0; Mismatches 0;
100.0%; Score 42; DB 8;
100.0%; Pred. No. 4.5e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 20
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                      ; Sequence 4, Application US/10645818; Publication No. US20040247620A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-645-818-1
; Sequence 1, Application US/10645818
; Publication No. US20040247620A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Bacteriophage MX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Bacteriophage MX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Conservative
```

us-10-645-818-5.rnpbm

```
ų
                                                                                                                                                                                                                                              US-10-795-159-492/c
; Sequence 492, Application US/10795159
; Publication No. US20050221439A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 771
SOFTWARE: PatentIn version 3.2
SEQ ID NO 575
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (5294)..(5294)
OTHER INFORWATION: n = a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (5156)..(5156)
OTHER INFORMATION: n = a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc feature
LOCATION: (5265)..(5265)
OTHER INFORMATION: n = a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (101)...(101)
OTHER INFORMATION: n = a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: H. influenzae
Query Match
Best Local Similarity
Them 36; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-795-159-575/c
                                                                                                                  ઠ
                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-795-159-201

Sequence 201, Application US/10795159

PUBLICATION NO. US20050221439A1

GENERAL INFORMATION:

APPLICANT: BAKALETZ et al.

TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE

FILLE REFERENCE: 28335/38815A

CURRENT APPLICATION NUMBER: US/10/795,159

CURRENT APPLICATION NUMBER: US 60/453,134

PRIOR APPLICATION NUMBER: US 60/453,134

PRIOR PILING DATE: 2003-03-06

NUMBER OF SEQ ID NOS: 771

SOOTWARR: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.1%; Score 32.4; DB 3; Length 657; Best Local Similarity 85.7%; Pred. No. 0.004; Matches 36; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                       APPLICANT: XU, H. HOWARD

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPRENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 05/99/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-65
PRIOR FILING DATE: 2000-12-67
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFFTMARE: PABLESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579 GACCTTGGCAAGGTCGTGCTTACCAACTGAGCTATTCCCGC 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGCTTGGGAAGCTCGTGTCTACCAACTGAGCTACCACCGC 42
                                                      Sequence 3781, Application US/09815242
Patent No. US20020061569A1
GENBRAL INPORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)....(657)
; OTHER INFORMATION: n = A,T,C or G
US-09-815-242-3781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Salmonella typhimurium
                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: H. influenzae
US-10-795-159-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                             US-09-815-242-3781/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 201
LENGTH: 1960
                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
GENERAL INCORMATION

GENERAL INCORMATION

GENERAL INCORMATION

TILLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE

FILE REPERENCE: 28335/38815A

CURRENT APPLICATION NUMBER: US 60/453,159

PRIOR PILIATION NUMBER: US 60/453,134

PRIOR PILIATION NUMBER: 2003-03-06

NUMBER OF SEQ ID NOS: 771

SOFTWARE: Patentin version 3.2

SEQ ID NO 492

LENGTH: 5436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 575, Application US/10795159
Publication No. US20050221439A1
GENERAL INFORMATION:
APPLICANT: BAKALETZ et al.
TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
FILE REFERENCE: 28335/38815A
CURRENT FILING DATE: 2004-03-05
PRIOR APPLICATION NUMBER: US 60/453,134
PRIOR FILING DATE: 2003-03-05
PRIOR FILING DATE: 2003-03-06
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
77.1%; Score 32.4; DB 9; Length 1960; 85.7%; Pred. No. 0.0046; Live 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 77.1%; Score 32.4; DB 9; Length 5436; Best Local Similarity 85.7%; Pred. No. 0.0052; Matches 36; Conservative 0; Mismatches 6; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5153 caccirioccaa dericerecireraccaa creacitar recede 5112
                                                                                                                                                    760 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
```

```
i LENGTH: 63563
i TYPE: DNA
i ORGANISM: Moraxella catarrhalis
US-10-672-787-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (93620)..(93620)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (93603)..(93603)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.7
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: H. influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (93620)..(93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-10-795-159-685/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33, Application US/10672787
Publication No US20040067554A1
GENERAL INDORMATION:
APPLICANT: LAGACE, Robert, E.
APPLICANT: PATTERSON, Chandra
APPLICANT: BENG, Kim, L.
APPLICANT: BENG, Kim, L.
APPLICANT: BENG, Kim, L.
APPLICANT: PATTERSON, Chandra
APPLICANT: PATTERSON, Chandra
APPLICANT: PATTERSON, CLANDES SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: ELITRA.025C1
CURRENT APPLICATION NUMBER: US/10/672,787
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 09/596,002
PRIOR APPLICANTON NUMBER: 2003-09-26
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL PROGETAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LAGACE, Robert, E.
APPLICANT: LAGACE, Robert, E.
APPLICANT: BATTERSON, Chandra
APPLICANT: BEGG, Kim, L.
TITLE OF INVENTION: UNCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: ELITRA, 0.25C1
CURRENT PELLIGN DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 0.9/596,002
PRIOR PALLING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 77.1%; Score 32.4; DB 7; Length 31147; Best Local Similarity 85.7%; Pred. No. 0.0065; Matches 36; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                      Length 28871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13927 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 13886
                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9246 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 9205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                 Score 32.4; DB 9;
Pred. No. 0.0065;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                  NAME/KEY: misc feature; LOCATION: (28833); CTHER INFORMATION: n = a, c, g, or US-10-795-159-575
                                                                                                                                      or
                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/10672787 Publication No. US20040067554A1
                                                                                                                                      ģ
                                                                                                                                                                                                                              ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                   77.1%;
                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (5660)
OTHER INFORMATION: n = a, c,
                                                                                NAME/KEY: misc feature
LOCATION: (82)...(82)
OTHER INFORMATION: n = a, c,
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.79
Matches 36; Conservative
                                        ORGANISM: H. influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-672-787-25/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-10-672-787-33/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q ID NO 25
LENGTH: 31147
LENGTH: 28871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-672-787-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
Sequence 684, Application US/10795159
Sequence 684, Application US/10795159
Publication No. US20050221439A1
GENERAL INFORMATION:
APPLICANT: BARALETZ et al.
TITLE OF INVENTION:
FILE REFERENCE: 28335/38815A
CURRENT APPLICATION NUMBER: US/10/795,159
CURRENT APPLICATION NUMBER: US/6/453,134
PRIOR PILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 771
SEQ ID NO 684
LENGTH: 417576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 685, Application US/10795159
Publication No. US2005022143941
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BAKALETZ et al.
TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE FILE REPERENCE: 28335/384815A
CURRENT APPLICATION NUMBER: US/10/795,159
CURRENT FILING DATE: 2004-03-05
PRIOR PILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                     ö
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.1%; Score 32.4; DB 9; Length 417576;
85.7%; Pred. No. 0.0091;
Live 0; Mismatches 6; Indels 0;
                                                     ö
Query Match 77.1%; Score 32.4; DB 7; Length 63563; Best Local Similarity 85.7%; Pred. No. 0.0072; Matches 36; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76404 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 76363
                                                                                                                                                  1051 GACCTTGGCAAGGTCGTCTTACCAACTGAGCTATTCCCGC 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // NAME/KEY: misc feature
// LOCATION: (138581)
// OTHER INFORMATION: n is a, c, g, or t
US-10-795-159-684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (93622)..(93625)
OTHER INFORMATION: n is a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ģ
```

```
ION: (29298)..(29298)
INFORMATION: n equals a, t, g or c
                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a, t,
FEATURE:
                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (653Ū9)..(65309)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a,
                                                                         NAME/KEY: misc feature
LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (80024)..(80024)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (44975)..(44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature LOCATION: (51805)..(51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10329670

Publication No. US20040018503A1

GENERAL INFORMATION:
Telaschmann et al.
TITLE OF INVENTION: Uncleotide Sequence of the Haemophilus influenzae Rd Genome, Fraggi TITLE OF INVENTION: Uncleotide Sequence of the Haemophilus influenzae Rd Genome, Fraggi TITLE OF INVENTION: Uncleotide Sequence of the Haemophilus influenzae Rd Genome, Fraggi TITLE OF INVENTION: Uncleotide Sequence of the Haemophilus influenzae Rd Genome, Fraggi TITLE OF INVENTION: UNCLEOTION NUMBER: US/10/329,670

CURRENT FILING DATE: 2000-08-23

PRIOR FILING DATE: 2000-08-23

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 1

SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.1%; Score 32.4; DB 9; Length 908766; Best Local Similarity 85.7%; Pred. No. 0.01; Matches 36; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      748266 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 748225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGCTTGGGAAGCTCGTGTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature

: LOCATION: (998604)..(998641)

: OTHER INCRAATION: n is a, c, g, or t

US-10-795-159-685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (292495)..(292495)
OTHER INFORMATION: n is a, c, g, or
                                                                                                                                                                                                                 or
                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (9223)..(9223)
OTHER INFORMATION: n is a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (4747) ...(4747)
OTHER INFORMATION: n equals a, t,
FEATURE:
NAME/KEY: misc feature
LOCATION: (9921)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Haemophilus influenzae FEATURE:
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (292404)..(292404)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                  FEATURE:
NAME/KRY: misc_feature
LOCATION: (39640)
OTHER INFORMATION: n is a, c,
SOFTWARE: Patentin version 3.2
SEQ ID NO 685
LENGTH: 908766
                                                                                 TYPE: DNA
ORGANISM: H. influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1830121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-329-670-1/c
```

셤 ઠે

100

us-10-645-818-5.rnpbm

NAME/KEY: misc feature LOCATION: (145171)..(145171) OTHER INFORMATION: n equals a, t, g or c υ υ g or c NAME/KEY: misc feature LOCATION: (105121)..(105121) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (120038)..(120038) JTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (122167)..(122167) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (139910)..(139910) OTHER INFORMATION: n equals a, t, g or g or g or FEMTURE:
NAME/KEX: misc\_feature
LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (119750)..(119750) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc\_feature LOCATION: (119824). (119924) OTHER INFORMATION: n equals a, t, g or FBATURE: g or NAME/KEY: misc feature LOCATION: (131340)..(131340) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (131360)..(131360) OTHER INFORMATION: n equals a, t, g or ö ö ö NAME/KEY: misc\_feature LOCATION: (140398)..(140398) OTHER INFORMATION: n equals a, t, g or FEATURE: ö NAME/KEY: misc feature LOCATION: (100091)..(100091) OTHER INFORMATION: n equals a, t, g מ מ ס NAME/KEY: misc feature LOCATION: (102696)..(102696) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (107248)..(107248) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (122336)..(122336) OTHER INFORMATION: n equals a, t, FEATURE: FEATURE:
NAME/KEY: misc\_feature
LOCATION: (145058). (145058)
OTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (121344)..(121344) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (142750)..(142750) OTHER INFORMATION: n equals a, FEATURE:

ö Gaps Query Match 77.1%; Score 32.4; DB 7; Length 1830121; Best Local Similarity 85.7%; Pred. No. 0.011; Matches 36; Conservative 0; Mismatches 6; Indels 0; ( 90995 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 90954 1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42 υ Search completed: January 10, 2006, 21:43:12 Job time : 836 secs ö or ö ö NAME/KEY: misc feature LOCATION: (145942)..(145942) OTHER INFORMATION: n equals a, t, g b g מ NAME/KEY: misc feature LOCATION: (150841)..(150841) OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEY: misc\_feature
LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEY: misc\_feature
LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (152530)..(152530) FEATURE: FEATURE: ð g

us-10-645-818-5

۲,

GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

January 10, 2006, 14:16:17; Search time 2184 Seconds (without alignments) 1093.143 Million cell updates/sec

US-10-645-818-5 42 Title: Perfect score: Sequence:

1 gagettgggaagetegtget.....accaactgagetaceacege 42 Scoring table:

5883141 segs, 28421725653 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

11766282 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

90 ba: \*
90 in: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AY297771 Myxococcu	AR619262 Seguence	AY247757 Bacteriop	AE016929 Bacteroid	AE017174 Porphyrom	AE001788 Thermotog	J01624 E.coli glyW	K01549 E.coli Gly-	AR449440 Sequence	X53236 E.coli glyv	AY657813 Synthetic	AF274339 Pseudomon	X52789 E.coli glyW	X53782 Haemophilus	X03239 E. coli gly	M12299 E. coli pgs	CQ872588 Sequence	AJ004950 Pseudomon
SUMMARIES	DB ID	1 AY297771	6 AR619262	7 AY247757	1 AE016929	1 AE017174	1 AE001788	1 ECOGLYW	1 ECOTRG3	6 AR449440	1 ECTRNAG3	11 AY657813	1 AF274339	1 ECTRNGCL	1 HIHPLATT	1 ECGLYWG	1 ECOPGSA	6 CQ872588	1 PPAJ4950
	% Nuery Aatch Length DB	360	4575	4581	300162	301933	9890	9/	9/	258	423	480	490	200	636	890	926	1960	2591
	% Query Match	100.0	100.0	100.0	86.2	86.2	82.4	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1
	Score	42	42	42	36.2	36.2	34.6	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4
	Result No.	1	7	m	4	ഗ	9 0	c 7	ω υ	6	c 10	11	12	c 13	14	c 15	c 16	17	c 18

AY379549 Thermus t AY379548 Thermus t CQ0372879 Sequence 166429 Sequence 3 173354 Sequence 3 173351 Sequence 3 173351 Sequence 3	மும் கூ	U32844 Haemophilus AE004687 Beeudomon AR008973 Sequence AR075314 Sequence	U32694 Haemophilus AE004708 Pseudomon U32698 Haemophilus D90832 E.coli geno AE008904 Salmonell AE008786 Salmonell	
AY379549 AY379548 CQ872879 I66429 I73354 I73351	AB088753 AE013664 PSEMETH AE013847	U32844 AE004687 AR008973 AR075314	U32694 AB004708 U32698 D90832 AE008904	CQ872962 AR408746 AX067450 AR408754 AX667458 AJ617740
4466644	-	0 0 1 1		100000
3286 3291 3291 5436 5559 5559	8232 8493 9117 10029	10668 10686 10763	11350 12542 13409 19662 20418	28871 31147 31147 63563 63563
1.77	77.1	77.1 77.1 77.1	1. 7. 7. 7. 1. 1. 7. 7. 7. 1. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7.	77.1.77
<i>c c c c c c c c c c</i>	55	<i>cc</i>	<i> </i>	77.
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	322.8 322.8 4.4.4.4	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	# # # # # # # # # # # # # # #
22222222222222222222222222222222222222	23 23 23 23 23	33 33 33 33 33 33 33 33 33 33 33 33 33	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	44444 0 11 12 12 12 12 12 12 12 12 12 12 12 12
υυυ	υυ	υ	ט ט ט	υυυυυ

# ALIGNMENTS

RESULT 1 AY29771 LOCUS DEFINITION MY ACCESSION AY VERSION AY VERYWORDS ACCESSION AY KEYWORDS ACCESSION AY KEYWORDS ACCESSION AY KEYWORDS ACCESSION AN ACCESSION A	AY297771 360 bp DNA linear BCT 27-OCT-2003 Myxococcus xanthus strain DZ1 tRNA-Gly gene, and bacteriophage Mx9 AX297711 GI:34229321
MSI	myxococcus xanthus Myxococcus xanthus Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterinese: Myxococcaese: Myxococcus.
REFERENCE 1 AUTHORS Ju	1 (bases 1 to 360) Julian, B.
Į.	į
PUBMED 14 REFERENCE 2 AUTHORS Ju	14553867 2 (bases 1 to 360) 2011ien.B.N.
	Direct Submission Submitted (13-MAY-2003) Kosan Biosciences, 3832 Bay Center Place, Januard CA 94545, 11SA
FEATURES source	Location/Qualifiers
	/organism="Myxococcus xanthus" /mol_type="genomic DNA" /strain="D21" /dh_xref="haxon.34"
tRNA	complement (133206) /product="tRNA-Gly"
misc_feature	
ORIGIN	
Query Match Best Local Similarity Matches 42; Conser	<pre>ch logic logi</pre>

1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42

ઠે

N

Page

셤

```
ATVNKTRSTGKTI I KAAQI NGEWGPYNPFGYLDREKEAKABELTLTJAAECRA'LIPHFR
ADRRREFLFQVFLGPRPGEEKALLKEDVDVEARTV I PRASNGRDTTKTGRERRVPVPD
ELMPYLLDDAWAASPSDILVPRAKGERGRADJYKMTRVI.RTALSAAGVVVGWDYI CRTQG
CGYRDVQSGGARQERRCPACDKRMWASGRPF PAVYGLRHTAATLHRKAGCDFLVI KU
VLGHAAVDTTDDVYTHLDEDYCRAELNKLSI.KAPPPPPTHQGGSDGGPDSGRUYYGEG
GTMHGLGDLQHHRARAWEARALPTELPPRNI.AGGI PAPLLSVKDVAASLSVSTAKVYQ
LLAAGVLPTWWQGSRRVKREDLDAYIARATGGKRGGK"
                                                                                                                                  /translation="WALKGASDATTNPSRLVQSVAAGPRATPWGVSASWYLLGRTATG
EYIVSSDAAKKGHPWATAAERLPTSPIDVNALALEVARLVALQQQSATPPSSGRTFGA
VADDWLITEAKRLVCPDNERRHLRHMBALWGWTDVELTPRVVKAHLAGLLKPEGPLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAR07018.1"
| Da.xref="GG1:379938860"
| translation="WRKRRWATRPPEDSPDTL.PDRFVLYVGRIPGGWSVSF81QGAP
| FVGSGRFGLLAAITGALKALARGGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /procedin id="AAP78668.2"
/db_xref="GI:37992882"
/translation="MSARERPILFSGAMVSAILAGRKTVTRRVLKPQPAPNSPHDGGT
/translation="MSARERPILFSGAMVSAILAGRKTVTRRVLKPQPAPNSPHDGGT
/translation="MSARERPILFSGAMVSAILAGRKTVTRRVLKPQPAPNSPHDGGT
REMANMEGALPKEHPGGMWVVLYRASYDGAD7AEERDFRWRPSIHMPRWASRLTLEVV
SVRAERLHALIDLPPEEVLABGLVRRQDGADDDPFRYRYGLPGHLTHRTGWAAFANLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="Aap78671.1"
/db_xref="G1:32264346"
/translation="WATCIGHUVTASGWRTATKALRLDASEVORVANLRWAKGRGLADF
/translation="WATCIGHUVTASGWRTATKALRLDASEVORVANLLSRPLWERHLAELA
TGPVTAXLLKSARLHTTPRLHGROVWWFGPAGCGSMALVYVELLSRPLWERHLAELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ^protein_id="AAP78667.1"
/db_xref="GI:32264342"
/translation="MSRCPEPLEPRFSRLVARGEPDACWLWQGRLDRNGYGRVAYRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLSAHRVAYELATGTRLLPSVLVCHHCDNRRCCNPAHLRAGTHADNNADMCAKGRQAR
GEGSTSKLTVAQVVELYRRRLAGESGPALAAAFGVSSRLVYLIAAGRKWAHVTQPVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MSPLKFKAMGKRGDAYEVRRDGVLLGQVLRVEMTKSVIGTNRAR
LSLVVRWNYRVEGIRITRGPYLTRQKAAEVLASQYDAHQRAKAVAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'tränglation="mtcpaprrnnrgmppsservvtprqaevlafvvtysdkhgyspa
padlcahfgwkstnacqdmltrlqdmhlltrapkvirslvvtesgreavaewrregeg
    'note="site specific recombinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERINGEASWDANPWVWAISFRRVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAP78670.1"
/db_xref="GI:32264345"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAP78669.1"
/db_xref="GI:32264344"
                                                                                           /protein_id="AAP78666.1"
/db_xref="GI:32264341"
                                                                                                                                                                                                                                                                                                                                                               2250. .2735
/codon_start=1
/transl_table=11
/product="Orf2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
/transI table=11
/product="Orf4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
/product="Orf6"
                             codon_start=1
transT_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
/product="Orf7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2967. .3695
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3961. .4275
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="Orf3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="Orf5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1272. .>4581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2761. .2970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .3964
                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                         PAT 14-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHG 27-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Characterization of the integrase gene and attachment site for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (27-OCT-2003) Kosan Biosciences, 3832 Bay Center Place,
Submitted A 94545, USA
Sequence update by submitter
On Oct 27, 2003 this sequence version replaced gi:32264340.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (03-MAR-2003) Kosan Biosciences, 3832 Bay Center Place,
Hayward, CA 94545, USA
3 (bases 1 to 4581)
Julien, B.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            no RNA stage; Caudovirales; Podoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                            1 (bases 1 to 4575)
Goldman, B.S., Hinkle, G.J., Slater, S.C. and Wiegand, R.C. Myxococcus xanthus genome sequences and uses thereof Patent: US 6833447-A 657 21-DEC-2004;
Monsanto Technology, LLC; St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY247757 4581 bp DNA linear PHG
Bacteriophage Mx9 integration region, partial sequence.
AY247757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 100.0%; Score 42; DB 6; Length 4575; Similarity 100.0%; Pred. No. 0.00013; 42; Conservative 0; Mismatches 0; Indels (
                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myxococcus xanthus bacteriophage Mx9
J. Bacteriol. 185 (21), 6325-6330 (2003)
14563867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .4581
/organism="Bacteriophage Mx9"
/mol_type="genomic DNA"
/db_xref="taxon:235265"
/note="integration region"
                                                                                                                              4575 bp Di
Sequence 657 from patent US 6833447.
AR619262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
/wol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, P22-like viruses.
                                                                                                                                                                                                       AR619262.1 GI:59723668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY247757.2 GI:37992881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          607. .2253 /
/gene="int"
607. .2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 4581)
Julien, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 4581)
Julien, B.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     607. .2253
/gene="int"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage Mx9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage Mx9
                                                                                                                                                                                                                                                                                              Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                   Unknown.
                                                                                                                                                                                                                                                                          Unknown
                           165
                                                                                                                                                       DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
AY247757
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                AR619262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMARK
                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
```

ORIGIN

δ 셤 ო

```
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product=rtwo-component system response regulator"
/product=rtwo-component system response regulator"
/protein_id="AAO75839_1"
/db_xref="G1:2338037"
/translation="MSKNDITVLIVEDELTLAMIIKDTLEENGFTIHTASDCEEGLHL
/ranslation="MSKNDITVLIVEDELTLAMIIKDTLEENGFTIHTASDCEEGLHL
/ranslation="MSKNDITVLIVEDELTLAMIIKDTLEENGFTIHTASDCEEGLHL
/ranslation="MSKNDIVENGFEMVRRIRGTDKGTPVLFLTARSAINDVVEGFELGAND
YLKKPPGMQELIIRIKALMGKAFSFTKTKVSSRFEIGSYLPDPVAQTLLHAGVRQELS
HERSEILKKLENRRQVVNTQDVLLELMGDDSFFNSRSLHVFITKLRHKLSQDEQIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="AAO75838.1"
/db_xref="G1:29338036"
/translation="MRKLIFLSLILSVGFASAQSEVPSDSIRRAPSSNIKEPGGFLL
DMGLMAVAPPRLD-PFSLDVPDVSKDYNQIFRLATDASYTQGFTDAFSSPFSGFGYGYG
WGLSSSPQFMQMGTFKLKNGWKINTYGDYDKDGWKVPNRSAMPWEKNNFRGAFELKSS
                                                                                                                                                                                                                                                               AE016929 300162 bp DNA linear BCT 28-MAR-2003
Bacteroides thetaiotaomicron VPI-5482, section 4 of 21 of the
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales; Bacteroidaceae; Bacteroides.

1 (bases 1 to 300162)

Xu, J., Bjursell, M.K., Himrod, J., Deng, S., Carmichael, L.K., Chiang, H.C., Hooper, L.V., and Gordon, J.I.

A Genomic View of the Human-Bacteroides thetaiotaomicron Symbiosis Science 299 (5615), 2074-2076 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu.7... Bjursell.M.K., Himrod, J., Deng, S., Carmichael, L.K., Chiang, H.C., Hooper, L.V. and Gordon, J.I.
Direct Submission
Submitted (31-0CT-2002) Department of Molecular Biology and Pharmacology, Mashington University in St. Louis, 660 S. Buclid, St. Louis, MO 63110, USA
Location/Qualifiers
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 300162
| Organism="Bacteroides thetaiotaomicron VPI-5482"
| /mol_type="genomic DNA"
| strain="VPI-5482"
| /m xref="taxon:226186"
| complement(106. .642)
| /locus_tag="BI0731"
                                                        ö
         Length 4581;
                                                        0; Indels
                                                                                                                         2000 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 2041
                                                                                                 42
                                                                                                 1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC
       100.0%; Score 42; DB 7; L
100.0%; Pred. No. 0.00013;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteroides thetaiotaomicron VPI-5482
Bacteroides thetaiotaomicron VPI-5482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (1553. .2932)
/locus tag="BT0733"
complement (1553. .2932)
/locus tag="BT0733"
/codon start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (106. 642)
/locus tag="BT0731"
/codon start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (845. .1540)
/locus_tag="BT0732"
complement (845. .1540)
/locus_tag="BT0732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGNFGIRIEVQQGRNGLY"
                                                                                                                                                                                                                                                                                                              complete genome.
AE016929 AE015928
AE016929.1 GI:29338035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "NVRGIGYKLIAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 300162)
                                                     Conservative
Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12663928
                                                                                                                                                                                                                 RESULT 4
AE016929
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
PUBMED
                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                             셤
```

```
/ trainiation="Martillilemywayasaqquotaqebadsuknvayidslyr
Elebywitgerpyvkaeqgktuyydprlusslpydnaydaytaydrgphililigg
QPVTVUNGKYTISVEQLSTLLKSMPOXERERAEVASAPARYQNGPPHILLIGG
QPVTVUNGKYTISVEGGLYTAKSWPUNER ERAEVASADLIYSYSYSBERRETDKEAL
HTLADGSVHPWNWYDITTSRHNNHQIRLGMDYAFTDKHLLSLVYTTAFTDVKPYATVT
GAQNYYDTSHSEGQLHNAKLDYQTPFGLKAGAEFTYYHAPGSQLLYSTLGEBTLNFLS
KDNQRINQMRINQMPYAGGCHTGADMGLNYGVATTALDNSYQMYFDPETETLLPDNNWQS
RREGOTLMPYAGGCHSTGTONYGVATTALDNSYQMYFDPETETLLPDNNWQS
RREGOTLMPYAGGCKSFGEGGTSTDVSTAABCYTTALDNSYQMYFDPETETLLPDNNWQS
RREGOTLMPYAGGSKSFGEGGTSTDVSTAABCYTTALDNSYQMYFDPETETLLPDNNWQS
RREGOTLMPYAGGSKSFGEGGTSTDVSTAABCYTTALDNSYQMYFDPETETLLPDNNWQS
YSRYWKRWQTYGYGSPERLVBIYKCPNFDFSBQGLVWVVPFKYKKWLDSRITAIGFR
YRQKDSDFWDIPFDRKLYTFVLTMNNTFTLSTRVDLKFTLSGFYQNKAITGFR
GNIDAALRYTPAKGSRAQULTKCDDIFNTSTISTNVRFGQQNVKNHYMKTTRAFGISFN
XFRGGXKEKKREBVDTSRFK"
                                                                                      /translation="mrkkskisiktirtimekkttgtvitknpakkmetisppeelknk
Liemadesikkmahtanagenpmiatereaffligktellegektygslebeiag
Liemadesikkmahtanagenpmiatereaffligktellegektygslebeiag
Liemadesikkmetagarliketynymmehaadpdrihemasvigdoy
pvpdrillhftelijoydendobrepekgtpolfpreggyamcyvpbslobrild
ggdsialmipvftpyieipebekgtpolfsredgymmygyddslobrild
gadsialmipvftpyieipebekgygdoyteisadowtydgiithpp
gkafilnpsnppsyklspetaarivnivkndnpmimiitddygygtpipkknpp
Hkaltyvssskyfgatgwrnavialhednivgnmialegyailnkryaslshp
ekwrt idralwdsgygtalmytagglslegogogowsleafakthar
hhalwdsgfflieddlraygygseidmlywakkfygdbffadytynpldyvprlan
etslyllingggproyskianlnbadyvkiggsikkvldbfyrbran"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
/producE="putative transport protein".
/producE="putative transport protein".
/protein_id="AA075843.1"
/db xref="G1:2338041"
/translation="MEWIINQLRDHPELAFFLTLFAGFWLGRFKIGKFSLGTVTSVLL VGLVGQLWGDTSSTOGPWGRAVEHLEFRFYGYKKGGPPFPGFRGLWGVVGFAVLNGTVSVLL VGLVGQLMGSTAGTAKTMGYNGGAGTLAGGGTISAVIGVASDTINQLSISDAQKATFINAIPY AYAVTYIFGTAGSAWILASLGPFWLGGLEKVKADCKELEAKWGTSEADBFGFYTALRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVFRAYKI DNEWFGKGKTVSELENYLVENDKRLFVERVRQKGVI EEVTPDMLLQPGDE VVLSGRREYATGEEDMIGPEVIDAQLLDFPAETLIPVMVTHRTPAGEKVSTI RALKFWH GVSI RSI RRAGINVPVLAGYVI DSGDILLELTGTKLEVETAAKQMGYI DR PTNQTDMI F VGLGILLGGIVVGALAHLGGI PI SLEYFGGAL I AGLVFEWLRSKHPFGGI PEPELWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNNVGLNMFTAVVGTAAGPSFVTGFKEVGFSLFIVGALATAIPLLSGLLMGRYLFKFH
PALTLGCTAGARTTTAALGAIQDALGSDTPALGYTVTYAVGNTLLIIMGVAIVLLM"
system sensor histidine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAO75841.1"
/db_xref="G1:29338039"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             decarboxylase AsdA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="aspartate decar
/protein_id="AAO75842.1"
/db_xref="GI:29338040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (5316. .6989)
/locus tag="BT0735"
complement (5316. .6989)
/locus tag="BT0735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus_tag="BT0736"
complement(7005. .8699)
/locus_tag="BT0736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (7005. .8699)
                                                                                                                                                                                                                                                                                                                                                                                                                      3201. .5309
/locus_tag="BT0734"
3201. .5309
/locus_tag="BT0734"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start≈1
/transl_table=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8906. .10573
```

```
complement (2613. 5435)
/locus tag="PG0553"
/locus tag="PG0553"
/locus tag="PG0553"
/note="aimilar to GB:M63420, GB:J03261, SP:P15018,
PD1:178415, PD1:187141, PD1:34362, and PLD:575489;
identified by sequence similarity; putative"
/codon start=1
/transI table=11
/product="extracellular protease, putative"
/protein id="AAQ65742.1"
/db_xref="GI:34396677"
/db_xref="GI:34396677"
THSFDDAMTIRLTPDFNPEDLIAQSRWQSQRDGRPVRIGQVIPVDVDFASKASHISSI
                                                          AE017174 301933 bp DNA linear BCT 02-SEP-2003
Porphyromonas gingivalis W83 section 3 of 8 of the complete genome.
AE017174 AE015924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [Dases 1 to 301933]
Nelson, K., Fleishmann, R., DeBoy, R., Faulsen, I., Fouts, D., Eisen, J., Daugherty, S., Dodson, R., Durkin, A., Gwinn, M., Haft, D., Kolonay, J., Nelson, W., White, O., Mas Durkin, L., Gray, J., Granger, D., Tettelin, H., Dong, H., Galvin, J., Duncan, M., Dewhirst, F. and
                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 301933)
Nelson, K., Fleishmann, R., DeBoy, R., Faulsen, I., Fouts, D., Eisen, J.,
Daugherty, S., Dodson, R., Durkin, A., Gwinn, M., Haft, D., Kolonay, J.,
Nelson, W., White, O., Mason, T., Tallon, L., Gray, J., Granger, D.,
Tettelin, H., Dong, H., Galvin, J., Duncan, M., Dewhirst, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="mayqskntdehvtfadallskryrkaondflngverlidmrpir
Tlinkkytkronaigapaydvillfrmllletwynlsdcaleerindsitfsrflglk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEBVSPDHSTISRFRSALTELGLMDKLLAQFNKQLSRHHISVREGVLVDASLVETPHK
WORTITIEREBERNEVSEREKEABEIDYÖKOVYRYRKKGTDEBERNWYSKOKRYHOGYKK
HCLTRWOGIVGKVITTAANRSDTKEFF PLLQGANIP POGTAVLADKGYACGENBSYLQT
HHLQDGIMHAQRNRALTEBEKQGNKALSPIRSTIERTFGSIRRWFHGGRCRYRGLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-OCT-2002) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1557. .2446
/note="miniature inverted-repeat transposable element"
/transposon="MITE_464.3"
complement(2613. .5435)
/locus_tag="PG0553"
complement(2613. .5435)
                                                                                                                                                                                                                                                                                  Bacteroidetes (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete Genome Sequence of the Oral Pathogenic Bacterium Porphyromonas gingivalis Strain W83
12949112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Porphyromonas gingivalis W83"
|mol_type="genomic DNA"
/strain="W83"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transposase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THTONILESIAFNLYRTPGIIMSSSLG"
                                                                                                                                                                                                                                                     Porphyromonas gingivalis W83
Bacteria; Bacteroidetes; Bacteroide
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (233. .1318)
Jocus tag="PG0549"
complement (233. .1318)
/locus tag="P60549"
/codon_start=1
/ransl_table=11
/prodvive______/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="ISPg1, transpoe
/protein_id="AAQ65741.1"
/db_xref="G1:34396676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:242619"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86. 1423
/insertion seq="IS1.4"
complement (233. 1318)
                                                                                                                                                                                                                           Porphyromonas gingivalis W83
                                                                                                                                                                      AE017174.1 GI:34396675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .301933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser, C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                               DEFINITION
                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                             RESULT 5
AE017174
                                                                                                                                         ACCESSION
                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                           SOURCE
                                                                                                                             /procein_id="AAO75846.1"
// db xref="G1:2933804"
/ translation="MKSDIEIARSCENKIKQVAESIGIPREEVENYGRYIAKIPEQL
/ translation="MKSDIEIARSCENKIKGNAESIGIPREEVENYGRYIAKIPEQL
IDEEKVKKKNIVIVTAITRAGIGKTTVSIGLAGLAKIGKKAIVALAREPSLGPCFG
MKGGAAGGGSYAQULPMEKINLHFTGDFHAITSAHNMISALLDNYLYQNQAKGFGLKEI
LMRRVLDNUDRSLRSIVVGLGPKSINGITGGSGFDITPASEIMAILLGSKOUFDLRRRI
ENILLGFTYDDQPFTVXCLGYAGAITVLLKDÄIHPNIVQTTGGTAAFVHGGPFRAITAH
GCNSILLATKLAMSFGDYVITRAGFGADLGAREKTVNIKCRKSGLQPKLTVIVATAQGLK
MHGGVSLDRIKEPNMEGLKGGLRNLDKHIRNLSFGQTVVVAFNKFATDTDEENEMLR
EHCEQLGVGTYAINNAFSGGGGGCAVDAARLVVOTIENNFSEPLRYTYKEBDSIQQKIEK
VATNLYGASVITYSSIARNRIKLIERMGITHYPVCIAKTQYSFSADPKIYGAVNNFFF
HIKDIVINGAGANTYAIAGEILRAMGITHYPVCIAKTQYSFSADPKIYGAVNNFFF
HIKDIVINGAGEILEMPGLPKEPQALHIDIVDGEIEGLS"

/ locus_tag="B10738"
// codon_etart=1
// codon_etart=1
// codon_etart=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
/product="hypothetical protein"
/product="hypothetical protein"
/protein_id="hypothetical protein"
/db_xref="G1:29338044"
/db_xref="G1:29338044"
/db_xref="G1:29338044"
/db_xref="G1:29338044"
/db_xref="MXILRNIILFGWALACTAFAQDRNADKVERPNTKKINFGIKAGFNSSMFWVSELKIKDVTIDEVQNNYKIGYFGAIFMRPNIKKHPIQPEASYNVSKGEIT
FDKLGSGHPALEDPDASAVGSVLHSIDFPILYOTNVVKKGPYGNSIFAGPKLRYLWGKO
NEITFTNFDQKGIHEKLYPLNVSVVIGVGVNISRIFFDFRYEQGIGNISKSIVYDNIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MKRDDLIPDIIEKEHQRQLKGIELIASENFVSDQVMQAMGSCLT
NKYAEGYPGKRYYGGCEVVDQSEQIAIDRLKEIFGAEWANVQPHSGAQANAAVPLAVL
NPGDKFMGLNLAHGGHLSHGSLVNTSGIIYTPCEYNLNQETGRVDYDQMEEVALREKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTHKTLRGPRGGVIMMGKDFPNPWGKKTPKGEIKMMSQLLDSAVFPGVQGGPLEHVIA
AKAVAFGEILQPEYKEYAKQVQKNAAILAQALIDRGFTIVSGGTDNHSMLVDLRSKYP
DLTGKVAEKALVSADITVNKNMVPFDSRSAFQTSGIRLGTPAITTRGAKEDLMIEIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="MIYPLPAILVSCGKDESEYNIITVAWTGTICTNPPMCYISVRPE
RHSYDIIKKNMEFVINLTTKDMAFPTDWCGVRSGRNYRKFEEMKLTPGRCTVVSAPLI
EESPLCIECRVKEIVSLGSHDMFIADVVNVRADDRNINPETGKFELAEANPLVYVHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KMIIGGGSAYSREWDYKRMREIADKVGAILMIDMAHPAGLIAAGLLENPVKYAHIVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 300162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                            'product="formate--tetrahydrofolate ligase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transI_table=11
/product="serine hydroxymethyltransferase"
/protein_id="AAOT5845.1"
/db_xref="GI:29338043"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIETVLSNVENEEVIAQVRARVNETMKKYPLFAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36.2; DB 1
Pred. No. 0.011;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDGSTGVSPIIFRRNDSALSFSFGFIL"
complement (13215. .13754)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="BT0740"
complement(13215. .13754)
/locus_tag="BT0740"
/locus_tag="BT0740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (12461. .13198)
/locus_tag="BT0739"
complement (12461. .13198)
/locus_tag="BT0739"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (13816. .14277)
/locus_tag="BT0741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (13816. .14277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein_id="AAO75847.1"
db_xref="GI:29338045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="flavoredoxin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYDLGEKIGKFGWSVEKKK"
                          locus_tag="BT0737"
                                                                                 table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1/transl table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.2%;
92.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGS
```

258334 AGCTIGGGAAGCIAATGCICTACCAACTGAGCTACTACCGC 258374

ò

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
ALENTROPEGADING LEGISTORY OF THE TRANSPORT LEGISTORY TO THE TRANSPORT OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAQ65744.1"
/db_xref="G1:34396679"
/tb_xref="G1:34396679"
/tb_xref=id1:34396679"
/tb_xref=id1:AABSGXVANKDGKRVWYPQTVASGRVIDTKRVARELAARSGASEGDYHGILHDLGIJVLRDYLSTGARVVLDGYGSFR.TANARGKGYBKKEDVSPRQFNSIRVAFYPEKRVNGSTHTTNVTLIDPNLRFVYKNPKDAAGNASSQTNTFDSPTPFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mokilssggussavunngtivoqagelpagttfftpmvlfqitsf
vtgqyymngmtkqinaalbkldtlibfykrermakikqsvslinknlsnkifsdbdlq
omkdvhsdlsiikneffedlscmtremskknkrnpwgrlkaaksiekekakfihkmbi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MCLORKONEVPVIRKGRLKSYWNTAFRGGFFLGLFVPLAALTKQ
SLLNGLLFGTAMIWAFVIVLWLCVGFTGSEYYRKQIKKLMSDQYAFLHED
SLLNGLLFGTPRVCPATYLYKKGYAKLERVVIIESPYREASEATDWDDLYGWSGE
YNFGDVHFBNHCAGFVPKDWRAPDFKANFDALITIFFERGLLFITKNDWESTFGQHSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLEVEALLYLTKYTELYMNIRYIQPDMRLINTLSALIELSTFREDDLFSMELINLHE
TVKKEILEYLSDLEKGPIFTSKIREIKSNFENSFVDIEEHKDNLLSEAKEIHKSTLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MDNQLLGFTSFVTAVNRYRLISQKIGLGGYIACPGYFY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="DNA-binding protein, histone-like family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus tag="PG0554"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7574. 8476

7574. 8476

710cus tag="PG0556"

760cus tag="PG0556"

760cs="identified by Glimmer2; putative"

7600n start=1

7600n start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="PG0557"
/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1

transl_table=11

/product="hypothetical protein"

/protein_id="AAQ6546.1"

/db_xref="GI:34396681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="AAQ65745.1"
/db_xref="GI:34396680"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="hypothetical protein"
/protein_id="AAQ65743.1"
/db_xref="G1:34396678"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (5962. .6480)
/locus_tag="PG0555"
complement (5962. .6480)
/locus_tag="PG0555"
/codon_start=1
/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEKDKMFVIDFRNGNLELYSSNDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (9756. .10577)
/locus_tag="PG0558"
complement (9756. .10577)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5761. .5877
/locus_tag="PG0554"
5761. .5877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8531. .9223
/locus_tag="PG0557"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGEQGSQGGGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAKDASRKNPQR'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
```

```
/translation="MKLQEQHYHEAASFLSSRLPGDAKTAIILGSGLGELAEKIENKT
VIPYNEIPHRAQATANGHKGNIIGGILGGTPVVAMQCRFHYEGSYMDQYTPEIRWKI
LLGIENLFVGNAAGGINTSFKVGDLMIICDHINNLPNPLIGPNMDMFGVRFPDMTRAY
DREFIAKAKGIAQEINIPWKEGVYVGLIGPSYETPAEYKFWGQVGGDAIGMSYTVPEVI
VARHTGIRVFGMSVITNEGYHPADDFVNDEQDVIRAANAASEKMGAIFARLIAAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MQPGYNGHGRGIYNFIGMTANRRSNLHNTVALDPDILTDTFQQC"
trānslation="MQPGYNGPPPALYARSYLYNR"
complement(11946. 13301)
/locus_tag="PG0561"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEVOI788 BCT 04-JUN-2004
Thermotoga maritima MSB8 section 100 of 136 of the complete genome.
AE001788 AE000512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDHLLQVGAQKAEVFQTPGNPVVYAERIMDPKAKTILVYAHYDVMPPEPLELWKSEPF
BPVIRDGHIWARGADDDKGQCMIQVKGFETALALGLVQCNVKFLFEGEEEIGSTNLEA
FCRAHKEMLSADVIIVSDTSMVSAETPSLTTGLRGLAVWEMEVTGPNRDLHSGHFGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VANPINELCKLIAGIVDENCRITIPHFYDDVVPLSDEERQMIAQVPPSEEKYCQALDI
DTVPGEAGYSTLERNSCRPSFDVCGIWGGYTGEGAKTVLPSKAYAKVSSRLVANQDHE
KISQMFIDYIRSVAPKHIKVKVTPLHGGEAYLCPIDLPAYKAAEEACTIAFGKRPLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNIRDYIRENEARFLEDLFALIRIPSVSAKSEHKPDMQRCAEHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (11946. .13301)
Jocus Laga PG0561.
/note="minimist GB: M96364, PID: 1033197, PID: 144480, and SP: QS9335; identified by sequence similarity; putative"
                                            /transT table=11
/product="purine nucleoside phosphorylase I, inosine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSSAVDTTIVDGKILMRGRKVPGEEAILAGAAEAAYKLMAKAHKTHE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.2%; Score 36.2; DB 1; Length 301933; 92.7%; Pred. No. 0.011; ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248859 AGCTTGGGAAGCTGATGCTCTACCAACTGAGCTACTACTACCGC 248899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="PG0560"
/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="peptidase, M20/M25/M40 family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/producte="hypochetical protein"
/protein_id="AAQ65749.1"
/db_xref="GI:34396684"
                                                                                                                                                                                                                                                                                                                     complement (10597. .11742)
/locus_tag="PG0559"
                                                                                                                                                                                                                                                                             complement (10597. .11742)
/locus_tag="PG0559"
                                                                                                              /protein_id="AAQ65747.1"
/db_xref="GI:34396682"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAQ65750.1"
/db_xref="GI:34396685"
/locus_tag="PG0558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="PG0560"
11719. ...11964
                                                                                             guanosine-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    table=11
                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11719. .11964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
AE001788/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
```

The state of the said

CDS

ø

```
/codon start=1
/transl_table=11
/product=hypothetical protein"
/protein_id="AAD16409.1"
/db_xref="GT:49D1897"
/translation="MSKMFITVFFGIMLVTVSLICIABTAPEIIWQKILGGSSDDYAF
svQQTPDGGYIVAGFTWSNDGDVSGHIGSLDAWIVKLDKDGNIEWQKTLGGSNNDWAF
svQQTPDGGYIVAGFTYSTDGVIRGHIGSLDAWVVKLDGNGNWQWQKTLGGSGNDWAT
svQQTTDGGYIVAGFTYSTDGVIRGHIGSLDAWVVKLGWQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
/transl_table=11
/producT="hypothetical protein"
/producT="hypothetical protein"
/producT="hypothetical protein"
/producT="hypothetical protein"
/db_xref="G1:4981899"
/tb_aref="G1:4981899"
/db_xref="G1:4981899"
/db_xref="G1:498
                                      EERIYNLLADHLLSQNPKFFIEVYGENMTVRCAEEDLHKTIRCPYCGNYLSIKESENT
LVPMKRYSGFCSNCHNVFDTESVHPPKYPEIVLVHEQPDRKIFYVKVWNENAHTTNNL
VCFNLMCENRSEMENIYLSRDFQVFTLEPGGEEKFEVEVALKRTDQRINKTYCLYVYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAGVILINSLSFLISGIFEMFIKVEEKHLKKVSKERNMWODIKSALLYIRSVRFILVT
ILVTAIMNFFTGSMHVLLPEHVSKLGKSEWYVGTLASMLSFGGLIVTFLMATIRTRAS
VKTLGLALVOYGLAVFVFAMTGNHWIMFAMYFLIGIFQTLFNINVITLLQLAIPEEMR
GKIFSLISAVSFSLLPVSYGFFGFLSSYVATAHIFITTSMALIAGGVLISLQRFEG"
complement (5371...6147)
/locus_tag="TM1337"
        RYFNMRKLELLGFRHKKIQNQVHDYFSKINEQTEVLDEANRNLKNFDLHRLSKNLSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSFLPAIIVSPFAGTVVDRHSRRNMMVVMDILRGVLFMYLFLMEYFSELTMALLLIV
TVLVSVFDSFFNPAVDSLLPDLVRKENLVRANSLYRLKNLSKILGPALGSLLLKVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
protein id="hAD36410.1"
/db_xref="GI:4981898"
/translation="MVVLYHKAPDMQNLLTSNLKAKNSLKASFPFCLNKKIIFHQYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MNRNLLLFASGSFVSLIGTRIYQVALAWWLYSKTGSSEYVGLFM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to percent identity: 0.00; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(6510. .6923)
/locus tag="TM1339"
complement(6510. .6923)
/locus tag="TM1339"
/locus tag="TM1339"
/notes="similar to percent identity: 0.00; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (5371. .6147)
/locus taga-raminar,
/note="similar to percent identity: 0.00; identified
sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                      /note="similar to GP:1800301 percent identity: 51.16; identified by sequence similarity; putative" (codon start=1 Crans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="TM1340"
/note="similar to GP:2815311 percent identity: 57.74;
identified by sequence similarity; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="permease, putative"
/protein_id="AAD36408.1"
/db_xref="GI:4981896"
                                                                                                                                                                                                                                               /locus_tag="TM1336"
3946. .5118
                                                                                                                                                                                                                                                                                                                                        locus_tag="TM1336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="TM1338"
6226. .6360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="TM1338"
/note="similar to |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6936. .7901
/locus_tag="TM1340"
6936. .7901
                                                                                                                                                                      FEDFNLSVSTYTFRLKNV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon start=1
trans table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .6360
                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Losos, L. Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J., Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J., Hafkey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A., McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D., White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M. Submitted (01-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                         Bacteria, Thermotogae, Thermotogales, Thermotogaceae, Thermotogae.

1 (bases 1 to 980).

Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J.,

McBon, M.E., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A.,

McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M.,

Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A.,

Richardson, D., Heidelberg, J., Sulton, G.G., Fleischmann, R.D.,

Eisen, J.A., White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRNVKRKRMKFLQAVSQIEGIYVPCIHGFFQTGMVKQTSPVDINEHPAHSIFVTKNTV
YEBRVFSIEVRRGTQRCRFCYMGHRLKPPRTLRMETFKKIVDLAIDQCNVEIIKLFY
EGLETRA VEHYLBYIIKKGGRVRIGSQRLEKLSKRIIETAAISGQRKTIVAPETSGRL
RKVIGKHEIKDESILEVVRISSLYGIDPGLYFILAIPGETFEDLDKIADLIMKVRHQ
MNKLKNTDGRLEIGINDLYPRPPTPFQYVKLPELKNIEDRFLYIVEKVKRGEPPVVIS
NDVVDEKVEKRQKDENENSLVKFETTVFHPISLLQPMISRGGLEIAFLLHYLHSKRF
NTVSDLENLLANEFGINAAMYFEEYIDKYCPWKIQKTLISEDYLLKEYFKALNFISTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MLEIVAFRGDEYGLSARILADFLDEFRIHEMSPDNFNGKEEIEN
DFIIVCNPKLLTENFLRQAYEYSRDSGIYFGYISALSIDLLREKLANYQEQISLDPOQ
YLIILRKENKSIKHRLNAEVFTRYESTVDNFPRVKHKKLCLSWYIDGNRFHLHISDGK
ICGINRDIPLEBIYRYPPDCQNCEYERYYAQDYQARGIFMDSCSSTLISTSEKGEYIN
VGNNPLKNAKVLISSYRPKQYNSEALLFHHISHGFBAGEVLYILNTNSYNHCSDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tränslation="MRTSLLYKIKEEERILPSKNLKGNEIIFILAFPDIYKYGLPNLG
IQTLYKELYIRDDVAVDRYYTDEDQPPSFEYGFKLKDSDFIGISFQYEGIVLNAFKIL
KAGSIPLINLLREENDPIIIGGGPVANYNPLPLSLVCDVIVLGEAEEAIHKIIDSYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PY ILYGFPNAKVTI PEKLEVDRLRMGKSEI VLEI DRI AGMRLLEI HAGEDI LNEVLKR
QFYVFSSDEI RKDVFYSVI PY PLKNSI KLFLYSWEEVNGPLRI VFGVGKRLREDVYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of Thermotoga maritima Nature 399 (6734), 323-329 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus tag="TW1334"
/note="similar to GB:AE000666 percent identity: 48.28;
identified by sequence similarity; putative"
/codon start=1
/transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="TM1335"
2002. .3930
/locus_tag="TM1335"
/note="gimilar to percent identity: 0.00; identified |
@equence_similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /producT="conserved hypothetical protein"
/protein id="AAD36406.1"
db_xref="GI:4981894"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .9890
/organism="Thermotoga maritima MSB8"
/mol_type="genomic DNA"
/strain="MSB8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transI_table=11
/product="hypothetical protein"
/protein id="AAD36407.1"
/db_xreff="GI:4991895"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECKLNCSQCFNRCIDISTTNYQGGMSNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:243274"
225. .2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus tag="TM1334"
225. .2009
                                                                                                                                Thermotoga maritima MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon start=1
trans1 table=1
    GI:4981893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002. .3930
                                                                        Thermotoga maritima
    AE001788.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBMED
REFERENCE
AUTHORS
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
```

ል

```
Murgoda, E.J.
Molecular mapping of glyW, a duplicate gene for tRNA3Gly of
Bacherichia coli
J. Bacteriol. 152 (2), 773-779 (1982)
6290450
Griginal source text: Escherichia coli DNA.
Griginal source text: Escherichia acoli DNA.
Griginal source text: Escherichia coli DNA.
Griginal source text: Escherichia coli of pgsA [1]. The order of
genes in this region is uvrC, pgsA, glyW, flaI. Comparison of the
order of determined restriction sites with the sites predicted from
transcription of glyW is counterclockwise on the circular E.coli
Tucker,S.D., Gopalakrishnan,A.S., Bollinger,R., Dowhan,W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="gly-tRNA-3 (glyW)"
10 bp upstream from AluI site; about 41.9 min on K12 map.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.1%; Score 32.4; DB 1; Length 76; 85.7%; Pred. No. 0.59; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                   1. .76
/organism="Escherichia o
/mol_type="genomic DNA"
/db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               <1. . > 76
/product="tRNA-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 36; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4941781
                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
ECOTRG3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                 trna
  AUTHORS
                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                              TITLE
                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                            RRARLSAGKVINDRIQCPFHGPEYDGNGRVRLIPALGKNYKVPDRFRVNSYPVYEKNN
II IMLMSGGEBERERKFRDJIDEDPAYAERRELMNVPFRAAVENQLDVWHLPPVHRTT
IGRGNRTLVHGPVVKMIDEDSPIFYVPNEVDRGQRVKRPEBLGGEBSRVYLEFIFPNL
WQNHISBGTRVVAFPVPUNGKYTMIYLRFYYKMTGLKPVDSIIARLSWPLNRIILHQD
RRVVETQERDIRKDVLVQGDLPIMEFRKRLYKEKKLIDFLFGGGQ"
                                         protein id="AAD36412.1"
/db_xref="GI:4981900"
/translation="MWFAVLSSNEVRRKPVGVRRLGRDLVFWRDSLGKVYALEDFCVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tränslation="MGGVKTYDPTSWRPKHLDLLLSAVIAFSLPAVAGWLYDLSGVLI
PMLIYYSLAWGLVKLRRGVVGYGTPPPKKPPKWFYVNVLVILTALFFAYQARIRVEEV
DRFGVLLTALLWAPVNASTEQILWLYLFDSWDLYPEKPRLRYRLQAWCSSPPSWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="MFWTKFLHVASPEGFFGVAFVLMTTISGFIHIVVWRQSGNMVFT
FIPHFLLANLGPLFWTGYSIVPYLWR"
                                                                                                                                                                                                                                                                                                     /locus tag="TM1341"
/note="similar to percent identity: 0.00; identified by
sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus_ga="TM1342"
/note="similar to percent identity: 0.00; identified by
sequence similarity; putative"
/codon start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus tag="TM1343"
//note="This region contains an authentic point mutation, causing a premature stop, and is not the result of a sequencing artifact; This region contains an authentic frame shift and is not the result of a sequencing artifact.; similar to PID:1088462 PID:1848058"
complement(91919..9267)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9413 AGCTTGGGAAGCTGGTGCTCTACCAGCTGACGCTACACCCGC 9373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34.6; DB 1;
Pred. No. 0.059;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                           /codon start=1

Lrans] table=11

/product="hypothetical protein"

/protein id="AAD36413.1"

/db_xref="GI:4981901"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                producT="hypothetical protein"
protein_id="AAD36414.1"
db_xref="GI:4981902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="codon recognized: AUG" 9373. .9445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (9194. .9267)
/locus tag="tRNA-Met-1"
/product="tRNA-Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="tRNA-Met-1"
                                                                                                                                                                                                                                                       /locus_tag="TM1341"
7903. .8376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="TM1342"
8385. .8594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .9036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8385. .8594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Conservative
                                                                                                                                                                                                                                     7903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
BCOGLYW/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                    CDS
```

ö

Gaps

ö

```
Contributed on tape April 1983 by M.Sprinzl & D.H.Gauss; from their contributed on tape April 1983 by M.Sprinzl & D.H.Gauss; from their entry 0730 in Nucleic Acids Res. 11, r1-r54 (1983). Instituted to tryptone. The authors further suggest a model in which three copies of a gene specifying Gly-tRNA-3 exist in close proximity. These copies are suggested to be identical. [1] was unable to detect 4-thiouridine in either the wild-type or Gly-tRNA-ins, although a consistent low yield of oligonucleotides containing 'us' suggestes that this base may be modified.
                                                                                                                                                                                       BCT 15-APR-1994
                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="codon recognized: GGC; Gly-tRNA-3 (NAR: 0730)"
                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="g in wild-type; t in Gly-tRNA-ins"
1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                           E.coli Gly-tRNA-3 with mutation Gly-tRNA-ins.
K01549.1 GI:174426
transfer pun.
                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Escherichia.

1 (bases 1 to 76)
Squires.C. and Carbon,J.
Normal and mutant glycine transfer RNAs
Nature New Biol. 233 (43), 274-277 (1971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .76
/organism="Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="tRNA"
/db_xref="taxon:562"
1. .76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="tRNA-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mod_base=d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mod_base=d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mod_base=d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trna
```

ازاد ماها مرابعا می ماها

A the time of the

ECUGLYW 76 bp DNA linear BCT 26-APR-1993 E.coli glyW gene, a duplicate gene for gly-tRNA-3, major species. J01624

Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae, Escherichia. 1 (bases 1 to 76)

glyW gene; transfer RNA; transfer RNA-Gly. Escherichia coli Escherichia coli

J01624.1 GI:146227

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

ò

REFERENCE

ò

```
gene="glyV(alpha)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . >480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brizuela, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brizuela, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sednences)
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
               trna
                                                            gene
                                                                                      trna
                                                                                                                                                            tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                 AY657813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 423)

Komine,Y., Adachi,T., Inokuchi,H. and Ozeki,H.

Genomic organization and physical mapping of the transfer RNA genes
in Escherichia coli K12
21 (4), 579-598 (1990)
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                             PAT 20-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCT 03-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECTRNAG3

E.coli glyV alpha, beta and gamma genes for tRNA-Gly.
X53236
X52236.1 GI:43151
Silv gene; transfer RNA gene; transfer RNA-Gly.
Escherichia coli
Interobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                        Breton, G.L.

Nucleic acid and amino acid sequences relating to M. catarrhalis
for diagnostics and therapeutics
Patent: US 6673910-A 104 06-JAN-2004;
Genome Therapeutics Corporation; Waltham, MA
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32.4; DB 6; Length 258;
Pred. No. 0.53;
0; Mismatches 6; Indels
                                                                                                                Score 32.4; DB 1; Length 76;
Pred. No. 0.59;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 GACCTTGGCAAGGTCGTGCTTACCAACTGAGCTATTCCCGC 154
                                                                                                                                                                         1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                          42 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .423
/organism=Escherichia coli"
/mol type="genomic DNA"
/db_xref="taxon:562"
/map="95min (4473Kb)"
/07. .182
                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                       258 bp Di
Sequence 104 from patent US 6673910.
AR449440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      AR449440.1 GI:42678497
            /mod_base=m7g
                                                                                                                77.1%;
85.7%;
                                                                     - /mod_base=p
5' end of mature tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.18;
                                        /mod base=t
                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 258)
                                                                                                                                             36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Unclassified.
                                                                                                                             Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  Unknown.
modified_base
                            modified base
                                                        modified_base
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                         LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECTRNAG3/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                 RESULT 9
AR449440
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
```

ઠે 셤

```
Direct Submission

Submitted (15-JUN-2004) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, Harvard Institute of
Proteomics, 320 Charles St., Cambridge, MA 02141, USA
This clone is part of the Pseudomonas aeruginosa PA01 ORF clone
collection generated by the Harvard Institute of Forteomics. Bach
CDS has been PCR-amplified from genomic DNA. Initiation codon has
been normalized to Arf and stop codon has been substituted for GGA
to allow generation of C-terminal tagged proteins. AttB
recombination sites have been added to either end of the orf and
directionally cloned using the Gateway cloning system into pDONR
201. Additional sequences in the clone: 'GAAGGAGATACC' before the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 bp DNA linear SYN 07-JUL-2004 Synthetic construct Peudomonas aeruginosa clone FLH045235.01F AX657813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
Loases 1 to 480)
Qiu,Q., Anumanthan,A., Mar,W., Zuo,D., Murthy,T.V.S., Hu,Y.,
Taycher,B., Halleck,A., Hainsworth,B., Lory,S., LaBaer,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qiu,Q., Anumanthan,A., Mar,W., Zuo,D., Murthy,T.V.S., Hu,Y.,
Taycher,B., Halleck,A., Hainsworth,B., Lory,S., LaBaer,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="Escherichia coli DH5alpha T1 resistant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.1%; Score 32.4; DB 1; Length 423; Best Local Similarity 85.7%; Pred. No. 0.5; Matches 36; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="derived from Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGGTATTCCCGC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGCITGGGAAGCICGTGCICTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Pseudomonas aeruginosa gene repository
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa ORF Project.
synthetic construct
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases I to 480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAT50088.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:32630"
/clone="FLH045235.01F"
                                                                                                                                                                                                                                                                        /gene="glyV(gamma)"
330. .405
/gene="glyV(gamma)"
/product="tRNA-Gly"
107. .182
/gene="glyV(alpha)"
/product="tRNA-Gly"
                                                                                                                                                                                 /gene="glyV(beta)"
/product="tRNA-Gly"
330. .405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                /gene="glyV(beta)"
219. .294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
/product="PA2819"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY657813.1 GI:49081053
```

misc\_difference 478. .479 /replace="ta"

Query Match 77.1%; Best Local Similarity 85.7%; Matches 36; Conservative

ઠે g

/replace="a"

misc\_difference 185 misc\_difference 403

```
RNA-Cys; transfer RNA-Gly; transfer RNA-Deu.
BSCheritchia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Bnterobacteriaceae; Bscherichia.
I (bases 1 to Scheritchia.
Komine, Y., Adachi, T., Inokuchi, H. and Ozeki, H.
Genomic organization and physical mapping of the transfer RNA genes in Escherichia coli Kl2
J. Mol. Biol. 212 (4), 579-598 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae genes for tRNA-gly, tRNA-leu and tRNA-lys and HPl host attachment site.
X53782.
X53782.
X53782.1 GI:43576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hauser, M.A. and Scocca, J.J.

Location of the host attachment site for phage HPl within a cluster of Haemophilus influenzae tRNA genes

Nucleic Acids Res. 18 (17), 5305 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-JUL-1990) Scocca J.J., Dept. of Biochemistry, Johns Hopkins Univ., School of Hygiene, 615 N. Wolfe Street, Baltimore, MD 21205, USA
Data kindly reviewed (08-OCT-1990) by Scocca J.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacteriophage attachment site; transfer RNA; transfer RNA-Gly; transfer RNA-Lus. transfer RNA-Lus. Haemophilus influenzae Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.1%; Score 32.4; DB 1; Best Local Similarity 85.7%; Pred. No. 0.49; Matches 36; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                       1. .500
/organism="Escherichia co
/organism="Escherichia co
/mol_type="genomic DNA"
/db_xref="taxon:562"
/map="42 min (2003Kb)"
/clone="340"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="tRNA-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="tRNA-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331. .417
/gene="leuz"
/product="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="leuz"
331. .417
                                                                                                                                                                                                                                                                                                                                                                                                                                            115. .190
/gene="glyW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115. .190
/gene="glyW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245. .318
/gene="cysT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="cysT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245. .318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scocca, J.J.
      X52789.1
                                                                                                                                                                                                                                                                                                                source
                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
HIHPLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRNA
    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           日
/db_xref="G1:49081054"
/translation="MRLKIQARSRQRPTTGTPRQSRLARASLHLFAAQRSRRPERILP
/translation="MRLKIQARSRQRPTTGTPRQSRLARASKGDDEQPGAQKRKK
GPCGREPRPPPPPMTHRASSARDFGRPRYRETAGLERQNEASKGDDEQPGAGKRKK
GPKALFSSTQAETWIMPGAGNETRTRDPDLGKIVLYQLSYSRVTTCCPPGRNFTFDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            490 bp DNA linear BCT 30-OCT-2000 Pseudomonas syringae pv. glycinea thermoresponsive genetic locus, mutant PG4180.617 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECTRNGCL 500 bp DNA linear BCT 03-JUN-2002 B.coli glyW, cysT, and leuZ genes for tRNA-Gly, tRNA-Cys and tENA-Leu. X52789
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="thermoresponsive genetic locus, mutant PG4180.617; similar to Erwinia chrysanthemi Orfl possibly encoding a cyclase involved in polyketide synthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 490)
Ullrich,M.S., Schergaut,M., Boch,J. and Ullrich,B.
Direct Submission
Submitted (02-JUN-2000) Ecophysiology, Max Planck Institute for terrestrial Microbiology, Karl-von-Frisch-Strasse, Marburg 35043, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas syringae pv. glycinea
Pseudomonas syringae pv. glycinea
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 490)
Ullrich, M.S., Schergaut, M., Boch, J. and Ullrich, B.
Temperature-responsive genetic loci in the plant pathogen
Pseudomonas syringae pv. glycinea
Microbiology 146 (Pt 10), 2457-2468 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.4; DB 1; Length 490;
Pred. No. 0.49;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                391 GACCTTGGCAAGATCGTGCTCTACCAACTGAGCTATTCCCGC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 389
                                                                                                                                                                                                                                                                                                                                                                         1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCGCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                     Score 32.4; DB 11;
Pred. No. 0.5;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
```

AF274339.1 GI:11037462

VERSION KEYWORDS SOURCE ORGANISM

AF274339

ACCESSION

DEFINITION RESULT 12 AF274339 LOCUS

11021922

JOURNAL PUBMED REFERENCE AUTHORS

JOURNAL

AUTHORS TITLE

REFERENCE

Query Match 77.1%; Best Local Similarity 85.7%; Matches 36; Conservative

ORIGIN

RESULT 13 ECTRNGCL/c LOCUS DEFINITION

g

ACCESSION

1. .490

misc feature

source

FEATURES

ö

Gaps

```
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECGLYWG

E. coli glyW region, a duplicated gene for tRNA-Gly-3.

X03239 M14391

X03239.1 GI:41604
Insertion sequence; inverted repeat; transfer RNA-Gly; unidentified reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
Bacherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pucker, S.D., Gopalakrishnan, A.S., Bollinger, R., Dowhan, W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular mapping of glyW, a duplicate gene for tRNA3Gly of
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 890)
Tucker, S.D. and Murgola, E.J.
Sequence analysis of the glyW region in Escherichia coli
Biochimie 67 (9), 1053-1057 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.4; DB 1; Length 636;
Pred. No. 0.48;
0; Mismatches 6; Indels
                                                             /db_xref="taxon:727"
/clone="piRc102 and subclones"
complement(125. .143)
/note="pot. transcriptional terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGCTIGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Data kindly reviewed (27-MAR-1986) by S. Tucker.
Location/Qualifiers
               'organism="Haemophilus influenzae"
                                                                                                                                  161. .342
/note="HP1 attB/attP common core"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53. .57 /note="imp. inverted repeat A"
                                                                                                                                                                                                                                                                                                                       'note="transcriptional start"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .890
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 152 (2), 773-779 (1982)
                                                                                                                                                                                                                                        330. .347
/note="HP1 attB sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31. .37
/note="pot. -10 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="pot. -35 sequence"
                                                                                                                                                                                                                                                                                                                                       complement (494. ..499)
/note="pot. -10 region"
complement (516. .521)
/note="pot. -35 region"
                             /mol type="genomic DNA"
/strain="Rd001"
                                                                                                                                                              complement (161.236)
/product="tRNA-Ly3"
complement (287..373)
/product="tRNA-Leu"
                                                                                                                                                                                                                                                                     complement (378. .453)
/product="tRNA-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <1. . 10
/insertion_seq="IS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 110 to 185)
                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6290450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_unit
                                                                                                  terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412
                                                                                                                                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                   CRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
ECGLYWG/c
LOCUS
                                                                                                                                                                   trna
                                                                                                                                                                                                                                                                     tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           유
```

```
/transl_table=11
/protein_id="CAA26984.1"
/brotein_id="GI:41605"
/db_xref="UniProt/Swiss-Prot:P06979"
/translation="WRTGPLABSELEWLDDILTKYNTDHALLDVAELDGLLTAVLSSP
QEIEPEQWLVAVWGGADYVPRWASEKEMTRAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                         'note="pot. transcription termination loop structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      note="unnamed protein product; unidentified reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Match 77.1%; Score 32.4; DB 1; Length 890; Local Similarity 85.7%; Pred. No. 0.47; les 36; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                note="mature transfer RNA-Gly-3"
                                                                                                                                              715. .220 inverted repeat B" note="imp. inverted repeat B" note="imp. inverted repeat B'"
                     'note="imp. inverted repeat A'"
                                                                                                                                                                                                                                                                   468. .475
/note="inverted repeat C'"
491. .496
/note="pot. -35 sequence"
514. .520
/note="pot. -10 sequence"
                                                                                                                                                                                                                            56. .463
note="inverted repeat C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: January 10, 2006, 18:22:11 Job time : 2188 secs
                                           10. .185
product="tRNA-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl
repeat_unit
                                                                                                     misc_signal
                                                                                                                                            repeat_unit
                                                                                                                                                                                     repeat_unit
                                                                                                                                                                                                                              repeat_unit
                                                                                                                                                                                                                                                                       repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Si
Matches 36,
                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                          promoter
                                         trna
```

.

GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

January 10, 2006, 10:49:30 ; Search time 484 Seconds (without alignments) 578.341 Million cell updates/sec

US-10-645-818-5 42 Title: Perfect score:

1 gagettgggaagetegtget.....aecaaetgagetaecaeege 42 Sequence:

IDENTITY NUC Scoring table:

4996997 segs, 3332346308 residues Gapop 10.0 , Gapext 1.0 Searched:

9993994 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

N\_Geneseq\_21:\*

geneseqn1980s:\* Database

genesequ2001bs:\* genesequ2002as:\* genesequ2002bs:\* genesequ2003as:\* genesequ2003bs:\* geneseqn2003ds:\* geneseqn2004as:\* geneseqn2004bs:\* geneseqn2003cs:\* geneseqn1990s:\* geneseqn2000s:\* geneseqn2001as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2005s:\*

SUMMARIES

Description	Adm36323 Bacteriop	Adm36321 Myxococcu	Adm36309 Bacteriop	Adm36306 Bacteriop	Adm36307 Bacteriop	Adm36304 Bacteriop	Ac164194 M. xanthu	Adl02418 DNA encod	Abd16247 Pseudomon	Aas51204 Salmonell	Abd16506 Pseudomon	Adt05165 Haemophil	Adt05456 Haemophil	Aaq55260 Restricti	Aat96101 Pseudomon	Aat99212 5.6 kb El	Aat90945 Ell genom	Aav06486 5.6 kb Ec	Aav39837 Pseudomon
ID	2 ADM36323	2 ADM36321	2 ADM36309	2 ADM36306	2 ADM36307	2 ADM36304	4 ACL64194	2 ADL02418	1 ABD16247	AAS51204	1 ABD16506	3 ADT05165	3 ADT05456	AAQ55260	AAT96101	AAT99212	AAT90945	AAV06486	AAV39837
* Query Match Length DB	42 1	74 1	257 1	360 1	360 1	1647 1	4575 1	258 1	549 1	657 4	1 069	1960 1	5436 1	5559 2	5559 2	5559 2	5559 2	5559 2	10763 2
& Query Match I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	77.1	77.1	77.1	77.1	77.1	77.1	17.1	77.1	77.1	77.1	77.1	77.1
Score	42	42	42	42	42	42	42	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4
Result No.	ਜ	υ υ	m	4	2	9	7	8	6	c 10	11	12	c 13	14	15	16	17	18	19

Aax99368 P. fluore	Adt05539 Haemophil	Aaf28538 Genomic f	Aaf28546 Genomic f	Aat42063 Haemophil	Continuation (2 of	Continuation (18 o	Continuation (39 o	Continuation (10 o	Adt05738 Haemophil	Adt05648 Haemophil	Adf03634 Bacterial	Continuation (6 of	Continuation (7 of	Continuation (12 o	Ada29439 DNA encod	Aaa81466 N. mening	Ac164415 M. xanthu	Aas59530 Propionib	Acf64459 Propionib	Continuation (3 of	Continuation (5 of	Continuation (8 of	Continuation (26 o	Continuation (26 o	Continuation (12 o	
AAX99368	ADT05539	AAF28538	AAF28546	AAT42063 00	AAT42063 01	AAT42063_17	ACF67367_38	ACF65388 09	ADT05738	ADT05648	ADF03634	ACF65384 5	ABA92787 6	ACF67367 11	ADA29439 _	AAA81466	ACL64415	AAS59530	ACF64459	AAA81489 2	AEB35724_4	AEB39174 07	AEB39175 25	AEB42401 25	AEB42737_11	
0	13	4	4	N	~	~	2	2	13	13	ដ	10	9	2	σ	ო	14	4	æ	ო	14	14	14	14	14	
.1 10763		.1 31147	.1 63563	.1 110000	.1 110000	.1 110000	.1 110000	.1 110000	.1 308766	.1 349980	.0 339	.0 30312	.0 40681	.0 110000	.1 282		.1 7035	.1 12531	.1 12531	1 110000	.1 110000	.1 110000	.1 110000	.1 110000	.1 110000	
77.1	77.1	77.1	77.1	77.1	77.1	77	77	77.1	77.1	77.1	71.0	71	71.0	71.0	67.1	67.1	67.1	67	67.1	67	67	67	67	67	67	
32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	29.8	29.8	29.8	29.8	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	
20	c 21	c 55	c 23	c 24	c 25	c 26	C 27	28	c 29	c 30	31	c 32	c 33	c 34	35	36	37	38	39	40	41	c 42	43	44	45	

### ALIGNMENTS

bacterial; bacteriophage Mx9; integrase; enzyme; int gene; Mx9 transformation system; Mx9 integrase; molecular biology; drug development; attP; attachment site; gene; ds. Bacteriophage Mx9 int gene attP core site SEQ ID NO:5. ADM36323 standard; DNA; 42 BP. 20-AUG-2003; 2003WO-US026413. (first entry) Bacteriophage Mx9. WO2004018635-A2. 03-JUN-2004 04-MAR-2004. ADM36323; ADM36323 

21-AUG-2002; 2002US-0405196P.

(KOSA-) KOSAN BIOSCIENCES INC.

Julien B;

WPI; 2004-226826/21.

Modifying a DNA of a bacterial cell comprises using an integrase gene a an attachment site for Myxococcus xanthus bacteriophage Mx9, useful in the fields of molecular biology and drug development.

Claim 5; SEQ ID NO 5; 37pp; English.

The present invention describes a method for modifying a DNA of a bacterial cell having in its genome a first attachment site recognised by a protein with Mx9 integrase activity comprises introducing an Mx9 transformation system into the cell, the system comprising a gene encoding a protein with Mx9 integrase activity protein operably linked to a promoter active in the host cell, and a DNA vector comprising a second

```
The present invention describes a method for modifying a DNA of a bacterial cell having in its genome a first attachment site recognised by a protein with Mx9 integrase activity comprises introducing an Mx9 transformation system into the cell, the system comprising a gene encoding a protein with Mx9 integrase activity protein operably linked to a promoter active in the host cell, and a DNA vector comprising a second attachment site recognised by the integrase protein, which may be the same as the first attachment site. Also described is a bacterial host cell produced by the method described above. The methods and compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying a DNA of a bacterial cell comprises using an integrase gene and an attachment site for Myxococcus xanthus bacteriophage Mx9, useful in the fields of molecular biology and drug development.
attachment site recognised by the integrase protein, which may be the same as the first attachment site. Also described is a bacterial host cell produced by the method described above. The methods and compositions of the present invention are useful in the fields of molecular biology
                                                                     and drug development, and particularly in transforming host bacterial cells using a bacteriophage Mys bystem. The present sequence represents the bacteriophage Mys int gene attP core attachment site, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial; Chrysoperla carnea; integrase; enzyme; int gene; Mx9 transformation system; Mx9 integrase; molecular biology; drug development; tRNAgly; 88.
                                                                                                                                                                                                Length 42;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                   1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                  1 GAGCTTGGGAAGCTCGTGCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                           Sequence 42 BP; 9 A; 14 C; 11 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                              100.0%; Score 42; DB 12;
100.0%; Pred. No. 2.2e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myxococcus xanthus tRNAgly nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KOSA-) KOSAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2003; 2003WO-US026413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-2002; 2002US-0405196P
                                                                                                                                                                                                                                                                                                                                                                                            ADM36321 standard; RNA; 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= |
49..65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10. .25
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27. .43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-226826/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myxococcus xanthus.
                                                                                                                                                                                                           Local Similarity
les 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004018635-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Julien B;
                                                                                                                                                                                                                                                                                                                                                                                                                             ADM36321;
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                           ADM36321/c
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                         RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                            88988888888888
                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                     ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for modifying a DNA of a bacterial cell having in its genome a first attachment site recognised by a protein with Mx9 integrase activity comprises introducing an Mx9 transformation system into the cell, the system comprising a gene encoding a protein with Mx9 integrase activity protein operably linked to a promoter active in the host cell, and a DNA vector comprising a second attachment site recognised by the integrase protein, which may be the aam as the first attachment site. Also described is a bacterial host cell produced by the method described above. The methods and compositions of the present invention are useful in the fields of molecular biology and drug development, and particularly in transforming host bacterial and drug development, and particularly in transforming host bacterial cells using a bacteriophage Mx9 system. The presents against a constant and constants and compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                  Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying a DNA of a bacterial cell comprises using an integrase gene and an attachment site for Myxococcus xanthus bacteriophage Mx9, useful in the fields of molecular biology and drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacteriophage Mx9 int gene attB2 site nucleotide sequence, which is used
of the present invention are useful in the fields of molecular biology and drug development, and particularly in transforming host bacterial cells using a bacteriology mys system. The present sequence represents Myxococcus xanthus tRNAgly nucleotide sequence, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage Mx9 integrase attB2 site nucleotide SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 42; DB 12; Length 257; 100.0%; Pred. No. 3.4e-07; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterial; bacteriophage Mx9; integrase; enzyme; int gene;
Mx9 transformation system; Mx9 integrase; molecular biology;
drug development; attB2; gene; ds.
                                                                                                                                                                        Length 74;
                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                      1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 257 BP; 54 A; 81 C; 82 G; 40 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                         42 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 1
                                                                                                                              Sequence 74 BP; 11 A; 22 C; 25 G; 0 T; 16 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the exemplification of the present invention.
                                                                                                                                                                      DB 12;
                                                                                                                                                                                           Pred. No. 2.5e-07
                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                        100.0%; Score 42;
100.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, SEQ ID NO 7; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KOSA-) KOSAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2003; 2003WO-US026413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-2002; 2002US-0405196P.
                                                                                                                                                                                                                                                                                                                                                                                                  ADM36309 standard; DNA; 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Conservative
                                                                                                                                                                                                                   42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-226826/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriophage Mx9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004018635-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM36309;
                                                                                                                                                                                                                                                                                                                                                            RESULT 3
ADM36309
                                                                                                                                                                                                                                                                                                                                                                                                                                          888888
                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                           ઠ
```

115 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 156

g

ઠે

ADM36306 standard; DNA; 360 BP

42

Bacteriophage Mx9 integrase attBl site nucleotide SEQ ID NO:3.

(first entry)

03-JUN-2004

ADM36306;

bacterial; bacteriophage Mx9; integrase; enzyme; int gene; Mx9 transformation system; Mx9 integrase; molecular biology; drug development; attB1; gene; ds.

Bacteriophage Mx9 WO2004018635-A2.

04-MAR-2004

```
bacterial cell having in its genome a first attachment site recognised by a protein with Mx9 integrase activity comprises introducing an Mx9 transformation system into the cell, the system comprising a gene encoding a protein with Mx9 integrase activity protein operably linked to a promoter active in the host cell, and a DNA vector comprising a second attachment site recognised by the integrase protein, which may be the same as the first attachment site. Also described is a bacterial host cell produced by the method described above. The methods and compositions of the present invention are useful in the fields of molecular biology and drug development, and particularly in transforming host bacterial cells using a bacteriophage Mx9 system. The present sequence represents a bacteriophage Mx9 system. The present sequence represents a bacteriophage Mx9 int gene att81 site mucleotide sequence, which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 360 BP; 65 A; 104 C; 126 G; 65 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 42; DB 12;
100.0%; Pred. No. 3.7e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM36307 standard; DNA; 360 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM36307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
ADM36307
ID ADM3
XX
AC ADM3
ઠે
```

Gaps

ö

Length 360; 0; Indels Bacteriophage Mx9

```
The present invention describes a method for modifying a DNA of a bacterial cell having in its genome a first attachment site recognised by a protein with Mx9 integrase activity comprises introducing an Mx9 transformation system into the cell, the system comprising a gene encoding a protein with Mx9 integrase activity protein operably linked to a promoter active in the host cell, and a DNA vector comprising a second attachment site recognised by the integrase protein, which may be the same as the first attachment site. Also described is a bacterial host cell produced by the method described above. The methods and compositions of the present invention are useful in the fields of molecular biology and drug development, and particularly in transforming host bacterial cells using a bacteriophage Mx9 system. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene attB2 site nucleotide sequence, which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modifying a DNA of a bacterial cell comprises using an integrase gene a an attachment site for Myxococcus xanthus bacteriophage Mx9, useful in the fields of molecular biology and drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                      Bacteriophage Mx9 integrase attB2 site nucleotide SEQ ID NO:4.
                                                                                       bacterial; bacteriophage Mx9; integrase; enzyme; int gene;
Mx9 transformation system; Mx9 integrase; molecular biology;
drug development; attB2; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial; bacteriophage Mx9; integrase; enzyme; int gene; Mx9 transformation system; Mx9 integrase; molecular biology; drug development; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 360 BP; 68 A; 110 C; 124 G; 58 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 GAGCTIGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriophage Mx9 int gene SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 4; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM36304 standard; DNA; 1647 BP
                                                                                                                                                                                                                                                                                                                                                     (KOSA-) KOSAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                             20-AUG-2003; 2003WO-US026413
                                                                                                                                                                                                                                                                                                                21-AUG-2002; 2002US-0405196P
                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacteriophage Mx9 int
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-226826/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                   Bacteriophage Mx9
                                                                                                                                                                                                    WO2004018635-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-2004
                                                                                                                                                                                                                                         04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                          Julien B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM36304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM36304
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modifying a DNA of a bacterial cell comprises using an integrase gene and an attachment site for Myxococcus xanthus bacteriophage Mx9, useful in the fields of molecular biology and drug development.
```

The present invention describes a method for modifying a DNA of a

Disclosure; SEQ ID NO 3; 37pp; English.

(KOSA-) KOSAN BIOSCIENCES INC. 21-AUG-2002; 2002US-0405196P. 20-AUG-2003; 2003WO-US026413.

WPI; 2004-226826/21

Julien B;

ô

```
The present invention describes a method for modifying a DNA of a bacterial cell having in its genome a first attachment site recognised by a protein with Mx9 integrase activity comprises introducing an Mx9 transformation system into the cell, the system comprising a gene encoding a protein with Mx9 integrase activity protein operably linked to attachment site recognised by the integrase protein, which may be the same as the first attachment site. Also described is a bacterial host cell produced by the method described above. The methods and compositions of the present invention are useful in the fields of molecular biology and drug development, and particularly in transforming host bacterial cells using a bacteriophage Mx9 system. The present sequence encodes bacteriophage Mx9 integrase, which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                            Modifying a DNA of a bacterial cell comprises using an integrase gene and an attachment site for Myxococcus xanthus bacteriophage Mx9, useful in the fields of molecular biology and drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic plant; DNA replication; gene regulation; gene expression; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1647 BP; 292 A; 528 C; 572 G; 255 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1394 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 42; DB 12; 100.0%; Pred. No. 5.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                               /product= "Mx9 integrase"
Location/Qualifiers
1. 1647
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; SEQ ID NO 1; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. xanthus DNA fragment, seg id 657.
                                                                                                                                                                                                               (KOSA-) KOSAN BIOSCIENCES INC.
                                                                                                                                              20-AUG-2003; 2003WO-US026413
                                                                                                                                                                               21-AUG-2002; 2002US-0405196P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACL64194 standard; DNA; 4575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-2001; 2001US-00902540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUL-2000; 2000US-0217883P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
Local 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-2005 (first entry)
                                                                                                                                                                                                                                                                              WPI; 2004-226826/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention.
                                                                                                                                                                                                                                                                                               P-PSDB; ADM36305
                                                                                 WO2004018635-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6833447-B1
                                                                                                                  04-MAR-2004
                                                                                                                                                                                                                                              Julien B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACL64194;
 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACL64194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
```

ö

Gabs

```
ö
                                                                                                                                                                                                                                  The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest. Sequences given in records for SEQ IDs 1-1849 represent a set of 1849 contig and singleton sequences comprising coding sequences, the genome of the bacterium Mycoccotus xanthus. Note: The sequence data for this patent did not form part of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a Moraxella catarrhalis polypeptide, useful for preparing a composition for diagnosing, preventing or treating infection caused by Moraxella catarrhalis.
                                                                                                                  New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4575 BP; 636 A; 1611 C; 1559 G; 769 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1981 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                             for this patent did not form part of the printed and obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 42; DB 14; 100.0%; Pred. No. 6.5e-07;
                                                   Wiegand RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a M. catarrhalis protein #104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; gene; Moraxella catarrhalis; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 104; 429pp; English.
                                                                                                                                                                                                       Example 1; SEQ ID NO 657; 25pp; English.
                                                 Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOME THERAPEUTICS CORP.
                 (MONS ) MONSANTO TECHNOLOGY LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-2000; 2000US-00540236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0128416P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL02418 standard; DNA; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-178127/17.
P-PSDB; ADL04338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6673910-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-2004
                                                   Goldman BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Breton GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL02418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL02418
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
```

.

ö

Gaps

```
The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bhind a P aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant or production of P. aeruginosa derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-Capanomona species using biochip technology. Sequences ABD01397-Capanomona species using biochip technology. Sequences ABD01397-Capanomona species data for this patent did not form part of the printed specification but was obtained in electronic format from USPFO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful as molecular targets for diagnostics, prophylaxis and treatment of
pathological conditions resulting from bacterial infection.
The invention relates to an isolated nucleic acid encoding an Moraxella catarhalis polypeptide. The nucleic acid is useful for preparing a composition for diagnosing, preventing or treating infection caused by Moraxella catarrhalis. The present sequence represents DNA encoding a M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial infection; gene; ds; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                          Score 32.4; DB 12; Length 258; Pred. No. 0.003; 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                        Sequence 258 BP; 82 A; 57 C; 44 G; 75 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa polynucleotide #14851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 14851; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rubenfield MJ, Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                  77.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00252991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0074788P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0094190P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABD16247 standard; DNA; 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                               catarrhalis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-615309/58.
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AB082676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6551795-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD16247;
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABD16247
នន្តន្តន្តន្តន
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS X C C C C C C C C C C C C X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
```

```
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes them to the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonalla typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids cands an also be used to identify proteins used in proliferation, to express these proteins, and to obtain the used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligonucleotide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                        Salmonella typhimurium cellular proliferation inhibitory sequence #102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                        Antisense; ss; prokaryotic cellular proliferation; antibiotic; antibacterial; drug design.
 Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        벙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.1%; Score 32.4; DB 4; Length 657;
85.7%; Pred. No. 0.0037;
live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 657 BP; 167 A; 140 C; 164 G; 183 T; 0 U; 3 Other;
                                     Indels
                                                                                                         478 GACCTIGGCAAGGICGIGCICIACCAACTGAGCTATICCCGC 519
                                                                       42
                                                                         GCTCTACCAACTGAGCTACCACCGC
Score 32.4; DB 11;
Pred. No. 0.0036;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3781; 511pp; English
                                                                                                                                                                                                   멾
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207727P.
23-0CT-2000; 2000US-0242578P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
77.1%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001WO-US009180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0191078P
                                                                                                                                                                                                 AAS51204 standard; DNA; 657
                                                                                                                                                                                                                                                                       (first entry)
                                                                       1 GAGCTTGGGAAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 36; Conserv
 Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
                                                                                                                                                                                                                                                                       13-FEB-2002
                                                                                                                                                                                                                                     AAS51204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                  AAS51204/c
                                                                                                                                                             RESULT 10
                                                                                                       셤
```

3

Sequence 549 BP; 122 A; 166 C; 166 G; 95 T; 0 U; 0 Other;

ADT05165 standard; DNA; 1960 BP

02-DEC-2004

ADT05165;

```
The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therappy of pathological conditions, as molecular tragets for diagnosities, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P aeruginosa nucleic acid, as components of effective antibacterial targets, as templates for antibacterial drugs, including anti-p. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using blochip technology. Sequences ABD01397-CABD17967 represent P aeruginosa polymucleotides of the invention. Note:

The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                   Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 690 BP; 149 A; 217 C; 214 G; 110 T; 0 U; 0 Other;
                     579 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 538
GAGCITGGGAAGCICGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bush D;
                                                                                                                                                                                                                                             Pseudomonas aeruginosa polynucleotide #15110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 15110; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segdata.uspto.gov/sequence.html
                                                                                                                               ABD16506 standard; DNA; 690 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00252991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0094190P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0074788P
                                                                                                                                                                                                        29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 85.7
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nolling
                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-615309/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ABO82935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rubenfield MJ,
                                                                                                                                                                                                                                                                                                        antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                               US6551795-B1
                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-2003
                                                                                                                                                                     ABD16506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                   ò
                                 음
```

```
ADT05456 standard; DNA; 5436 BP
                                                                                                                                                                                                                                                                                                                                            05-MAR-2004; 2004WO-US007001.
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                              Haemophilus influenzae
                                                                                                                                                                                                                                                                                WO2004078949-A2
                                                                                                                                        02-DEC-2004
                                                                                                                                                                                                                                                                                                              16-SEP-2004
                                                                                                         ADT05456;
                                                                                                                                                                                                                      contig
                                                               ADT05456/
g
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                77.1%; Score 32.4; DB 11; Length 690; 85.7%; Pred. No. 0.0038; tive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                               1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
```

RESULT 12
ADT05165

ò

```
New polynuclectides of nontypeable strain of Haemophilus influenzae, useful for treating or preventing NTHi bacterial infections of the middle ear and/or nasopharynx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises nucleotide sequences (genes) from the genome of nontypeable strain of Haemophilus influenzae (NTH1). The NTH1 DNA sequences of the invention are useful for treating or preventing NTH1 bacterial infections of the middle ear and/or nasopharynx. The present nucleic acid represents an NTH1 contig sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                da;
                                                                                                                                                                                                                                                                        middle ear bacterial infection; nasopharynx bacterial infection; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             middle ear bacterial infection; nasopharynx bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae (NTHi) contig DNA sequence - SEQ ID 492.
                                                                                                                                                                                                      Haemophilus influenzae (NTHi) contig DNA sequence - SEQ ID 201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.1%; Score 32.4; DB 13; Length 1960; Best Local Similarity 85.7%; Pred. No. 0.0048; Matches 36; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1960 BP; 603 A; 371 C; 394 G; 592 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  760 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 201; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dyer DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIL-) CHILDRENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAR-2004; 2004WO-US007001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAR-2003; 2003US-0453134P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAR-2003; 2003US-0453134P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bakaletz LO, Munson RS,
                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-662422/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004078949-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-2004
                                                                                                                                                                                                                                                                                                                 contig.
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE STANTAGE STANTAGE
```

```
WPI; 1994-035067/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-558141/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in Pseudomonads
                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-1994;
                                                                                                                                                                                                                                                                                                                             31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                       US5686282-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-1997
                                   organisms
                                                                                                                                                                                                                                                                                                            AAT96101;
                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                   AAT96101
셤
                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                   ö
                                                    New polynucleotides of nontypeable strain of Haemophilus influenzae, useful for treating or preventing NTHi bacterial infections of the middle ear and/or nasopharynx.
                                                                                                        The invention comprises nucleotide sequences (genes) from the genome of nontypeable strain of Haemophilus influenzae (NTHi). The NTHI DNA sequences of the invention are useful for treating or preventing NTHi bacterial infections of the middle ear and/or nasopharyux. The present nucleic acid represents an NTHi contig sequence of the invention.
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                 Gene activation; gafA; transcriptional activator; activator; sensor; regulation; induction; biocontrol agents; crop protection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Becker J;
                                                                                                                                                                              ch 77.1%; Score 32.4; DB 13; Length 5436; 11 Similarity 85.7%; Pred. No. 0.0061; 36; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                              Sequence 5436 BP; 1705 A; 1150 C; 884 G; 1691 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                 Restriction fragment comprising gene activating sequence.
                                                                                                                                                                                                                               5153 GACCTTGGCAAGGTCGTCTACCAACTGAGCTATTCCCGC 5112
                                                                                                                                                                                                                    1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stein JI, Howell CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trag= b
/label= ORF 2.
/label= GRP 2.
/rag= c
/label= glyW
/note= "tRNA coding sequence."
/rtag= d
/label= ORF 3.
                                                                                        Example 1; SEQ ID NO 492; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                  Munson RS, Dyer DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/label= ORF 1.
1906. .3633
                                                                                                                                                                                                                                                                                   AAQ55260 standard; DNA; 5559 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lam ST, Hill DS,
(CHIL-) CHILDRENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-US006300.
                                                                                                                                                                                                                                                                                                                                                                                                                        210. .1688
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas fluorescens.
                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIBA ) CIBA GEIGY AG.
                                  WPI; 2004-662422/64
                                                                                                                                                                                         Local Similarity
                  Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaffney TD,
Ligon JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9401561-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-1992;
                                                                                                                                                                                                                                                                                                                      25-MAR-2003
                                                                                                                                                                                                                                                                                                                               28-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JAN-1994
                                                                                                                                                                                                                                                                                                     AAQ55260;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                RESULT 14
 SXCCCCCXXXTTTXXXXCCCCXXX
                                                                                                                                                                                                                      ઠે
```

. . . .

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a Pseudomonas fluorescens lemA gene fragment. The P. fluorescens lemA gene, or lemA derivatives with enhanced gafA kinase activity, can be used to increase the production of biocontrol factors, e.g. chitinase, gelatinase, pyrrolnitrin and cyanide in Pseudomonads,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas fluorescens lemA gene - useful for activating gene expression
Gene activating sequences, partic. from pseudomonas - used for inducing expression of genes which are latent or expressed at low levels in target
                                                                                                                                                                                                                 The gene activating sequence is contained within an 11 kilobase EcoRI fragment (E11) from P. fluorescens. DNA sequence analysis of E11 has identified five open reading frames (ORF), of which ORFs and ORF 2 share significant homology with numerous activator and sensor components respectively of bacterial two-component regulatory systems. The gene activating sequences can be used in microorganisms to induce the production of gene products and secondary metabolites. They are used particularly for production of bacterial blocontrol agents for use in inhibiting plant pathogens. This sequence is a fragment of E11. See also AAQ55261. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lemA gene; gafA kinase; biocontrol factor; production; chitinase; gelatinase; pyrrolnitrin; cyanide; Pseudomonad; biological control; pathogenic fungus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5559 BP; 1194 A; 1743 C; 1637 G; 984 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4650 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGCTTGGGAAGCTCGTGTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 77.1%; Score 32.4; DB 2;
Best Local Similarity 85.7%; Pred. No. 0.0061;
Matches 36; Conservative 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas fluorescens lemA gene fragment.
                                                                                                                                                        Disclosure; Page 71-74; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Col 41-45; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-00570184.
92US-00908284.
93US-00087636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVS ) NOVARTIS FINANCE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT96101 standard; DNA; 5559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00459701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00287442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-00258261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas fluorescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lam ST, Gaffney TD;
```

```
thus rendering them more effective for the biological control of pathogenic fungi
                                                          Sequence 5559 BP; 1194 A; 1747 C; 1633 G; 984 T; 0 U; 1 Other;
             ឧឧ
```

; 0 Gaps ő Query Match
77.1%; Score 32.4; DB 2; Length 5559;
Best Local Similarity 85.7%; Pred. No. 0.0061;
Matches 36; Conservative 0; Mismatches 6; Indels 0;

1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGACTACCACGC 42

ઠે Ωp Search completed: January 10, 2006, 17:45:34 Job time : 487 sec8

: 1

À.
120
H
4.
r.,~
æ
ĭ
8
'n
4
ò
ī
$\overline{}$

26.8 63.8 946 26.6 63.3 440 26.6 63.3 740	26.6 63.3 748 10 CW807574 26.6 63.3 942 9 BH138539 26.4 62.9 593 9 AZ293626 0 26.4 62.9 623 9 AZ293626 1 26.2 62.4 191 9 AZ570476 2 6 61.9 540 10 CW016252	26 61.9 545 9 26 61.9 554 9 26 61.9 627 9 26 61.9 657 9 26 61.9 720 10	26 61.9 744 10 AGA12442 26 61.9 865 1 AV98406 26 61.9 129 10 AG429224 25.8 61.4 547 10 CW873528 25.6 61.0 375 5 BY022217	61.0 489 9 AZZ91650 61.0 574 9 AZ632374		RESULT 1 CL688860/c CL688860 760 bp DNA linear GSS 09-JUL-2004 LOCUS DEFINITION PRI014c_F06_2 - PRI014c.BR (760) Mixed stage fosmid library of P. PACCESSION CL688860 VERSION CL688860.1 GI:50197938 KEYWORDS SOURCE Pristionchus pacificus ORGANISM Pristionchus pacificus ORGANISM Pristionchus pacificus	Eukaryota, Metazoa, Nematoda, Chromad Neodiplogasteridae, Pristionchus. 1 (bases 1 to 760) Srintvasan, J., Otto, G.W., Kahlow, U., AppaDB: an AcedB database for the nem Pristionchus pacificus	JOURNAL NUCLEAR ACIDS KES. 32 (1), D421-D422 (2004) PUBMED 14681H-SOMMERT Contact: Sommer RJ COMMENT Contact: Biology Max-Planck-Institute for Developmental Biology	Tel: 00497071601371 Fax: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech sequenced at Vancouver, Canada. Seq primer: Tries Class: Location/Qualifiers	Source / Organism="Pristionchus pacificus" /mol type="genomic DNA" /strafin="claifornia" /db xref="taxon: 54126" /clone lib="Mixed stage fosmid library of P. pacificus var. California" /note="Vector: pEpifos-5 Fosmid vector"	Query Match 77.1%; Score 32.4; DB 10; Length 760; Best Local Similarity 85.7%; Pred. No. 0.088; Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: January 10, 2006, 16:47:24 ; Search time 3793 Seconds (without alignments) 518.075 Million cell updates/sec	8-5 agctcgtgctaccaactgagctaccaccgc 4	d: umber	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	LS	`` <b>L</b> . 0	SUMMARIES  Regult Query  No. Score Match Length DB ID Description	32.4 77.1 760 10 CL688860 32.4 77.1 773 10 CL692030 32.4 77.1 802 9 BZS64906 32.4 77.1 811 10 CL664382 32.4 77.1 1250 9 BZS63705 32.4 77.1 1250 9 BZS637553 32.4 77.1 1393 9 BZS77553	.3 665 5 BU702692 .3 665 6 BU702692 .3 719 6 CF725482 .3 729 6 CF732823 .0 427 11 P862R .0 503 2 BR43009 .1 696 9 BH163135	27.6 65.7 692 10 AG391506 27.2 64.8 606 8 CX096269 C 27.2 64.8 708 9 CC822117 C 26.8 63.8 180 9 AZ608686 A 26.8 63.8 312 9 AZ945284 A

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

JOURNAL PUBMED COMMENT

REFERENCE AUTHORS TITLE

LOCUS DEFINITION CL692030/c

RESULT 2

```
GSS 17-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M., Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
Bacteria, Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 806)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BZ551245
pacs1-60_3056.y2 pacs1-60 Pseudomonas aeruginosa genomic clone pacs1-60_3056, genomic survey sequence.
                                                                                                                                                                                                                                                                                                              /db_xref="taxon:287"
/clone="paca2-164 4981"
/clone=lib="paca2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:287"
-Clone="pacal-60"
|Clone lih="pacal-60"
|note="clinical isolate 1-60 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 77.1%; Score 32.4; DB 9; Length 806; Similarity 85.7%; Pred. No. 0.088; 36; Conservative 0; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.1%; Score 32.4; DB 9; Length 782; Best Local Similarity 85.7%; Pred. No. 0.088; Matches 36; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGCTTCGGAAGCTCGTGCTCTACCAACTGAGCTACCACGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
                                                                                                                                                                                                                                               aeruginosa"
                      Genome Center
University of Washington
Dox 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 2066857244
Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                                                      1. .782
/organism="Pseudomonas
                                                                                                                                                                      Class: shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
     Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BZ551245.1 GI:27154826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BZ551245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S:
Matches 36
                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
BZ551245/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                   CL692030 173 bp DNA linear GSS 10-JUL-2004 PRI0158a_A12_2 - PRI0158a_BR (773) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 17-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BZ564906 782 bp DNA linear GSS 17-DEC-20
pac82-164 4981.x1 pac82-164 Pseudomonas aeruginosa genomic clone
pac82-164-4981, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spenanustr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601398
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. 773
//crganism="Pristionchus pacificus"
//crganism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 782)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, T.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 773)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32.4; DB 10; Length 773;
Pred. No. 0.088;
0; Mismatches 6; Indels 0
331 GACCTIGGCAAGGTCGTGCTCTACCAACTGAGGTATTCCCGC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/strain="California"
                                                                                                                                                                                                                                                                                          CL692030.1 GI:50213938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BZ564906.1 GI:27191664
                                                                                                                                                                                                                                                                                                                                          Pristionchus pacificus
Pristionchus pacificus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 77.1%;
1 Similarity 85.7%;
36; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Sommer RJ
                                                                                                                                                                                                                                       survey sequence.
CL692030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14681447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BZ564906
```

FEATURES

ORIGIN

ö

Gaps

ö

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

ACCESSION

BZ564906/c LOCUS

RESULT 3

g

ö

Gaps

ന

ö

Gaps

셤

```
BZ577553 17-DEC-2002 msh2_5462.x1 msh Pseudomonas aeruginosa genomic clone msh2_5462,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae; Pseudomonas.

(bases 1 to 1393)

Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                               /db_xref="taxon:287"
/clone="pac82-164 4385"
/clone=lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xrefe"taxon:287"
/clone="msh2_5462"
/clone_lib="msh"
/note="Environmental isolate. Whole genomic shotgun
library."
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                              77.1%; Score 32.4; DB 9; Length 1250; 85.7%; Pred. No. 0.093; 1ve 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.1%; Score 32.4; DB 9; Length 1393; 85.7%; Pred. No. 0.094; cive 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 GACCTIGGCAAGGICGIGCTCTACCAACTGAGCTATIGCCGC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                1. .1250
Corganiam="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Pseudomonas aeruginosa"
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 206857244
Email: craymond@u.washington.edu
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="MSH"
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BZ577553.1 GI:27212614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                          36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BZ577553
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                         GSS 09-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 17-DEC-2002
                                                                                                  CL664382 811 bp DNA linear GSS 09-JUL-2004
PRI0146d_G08 - PRI0146d.B21 (811) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1250 bp DNA linear GSS 17-DEC-20 pacs2-164 4385.y2 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164 4385, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spencer, D.H., Raymond, C.K., Smith, B.B., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. pacificus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 811)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R., AppanB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: 17
Seq primer: Comid ends.
Class: Location/Qualifiers
                                                                                                                                                                                                                                                   Pristionchus pacificus
Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32.4; DB 10; Length 811;
Pred. No. 0.088;
0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:54126"
/db_xref="taxon:54126"
/db_main="mixed stage fosmid library of var. California"
/note="Vector: pEpifos-5 Fosmid vector"
384 GACCTTGGCAAGGTCGTGCTCTACCAACTGAGCTATTCCCGC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  706 GACCTIGGCAAGGICGIGCTCIACCAACIGAGCIAITCCCGC 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemanustr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                              CL664382.1 GI:50154798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BZ563705.1 GI:27188137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.18;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Conservative
                                                                                                                                                                    survey sequence.
CL664382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                               RESULT 5
CL664382/c
                                                                                                                        DEFINITION
                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
BZ563705/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
```

ઠે

ö

The state of the s

```
BU702692.1 GI:23627751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                        POLYA=No.
                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU702692
                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

8 Csiurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 556)

8 Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., VanBuren, V., Falco, G., Martin, P.R., Stagg. C.A., Basesy, U.C., Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagrasinger, D., Keller, M., Kelso, E., Kelsoe, G., Umezawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.

Transcriptone analysis of mouse stem cells and early embryos PloS Biol. 1 (3), 410-419 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                           GSS 17-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 18-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E0352G09-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus musculus cDNA clone NIA:E0352G09 IMAGE:30863984 5', mRNA sequence. CN694592
                         msh2 4612.x1 msh Pseudomonas aeruginosa genomic clone msh2_4612,
genomic survey sequence.
                                                                                                                                                                               Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                Sims, E.E., Hastings, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:287"
/clone="msh2_4612"
/clone_lib="msh"
/note="Environmental isolate. Whole genomic shotgun
library.
                                                                                                                                                                                                                                         1 (bases 1 to 1635)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings
Burns, J.L., Kaul, R. and Olsen, M.V.
Mhole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32.4; DB 9; Length 1635; Pred. No. 0.095; 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 GACCTIGGCAAGGICGIGCTCIACCAACTGAGCIAITCCCGC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aeruginosa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                     Genome Center
Universelty of Washington
Universelty of Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 206687244
Email: craymond@u.washington.edu
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pseudomonas a
/mol_type="genomic DNA"
/strain="MSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                        GI:27210816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CN694592.1 GI:47463341
                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 j. .1635
                                                                                               BZ575755
BZ575755.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 8
BZ575755
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CN694592
                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
```

```
/Longe // Jobbs // Jobs // J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU/UZ692
UI-MENA linear EST 15-JUL-2003
UI-MENAP_FC0-bzb-p-24-0-UI.rl NIH_BMAP_FC0 Mus musculus cDNA clone
IMAGE:6401543 S', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.
Sciurognathi; Muroidea; Murinae; Mus.
I (bases 1 to 665)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="NIA Mouse E10.5 whole embryo cDNA library (Long)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="niaEST:E0352G09-5"
db_xref="naxon:10090"
|Clone="NIA:E0352G09 IMAGE:30863984"
| tissue_type="whole embryo including extraembryonic tissues at 10.5-days postcoitum"
| dev stage="E10.5"
| lab_host="DH10B"
Laboratory of Genetics
National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0352_row: G_column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.3%; Score 30.8; DB 7; Length 556; Best Local Similarity 83.3%; Pred. No. 0.36; Matches 35; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .556
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                             Seg primer: M13 Reverse
High quality sequence stop: 556
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
```

us-10-645-818-5.rst

```
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/mousefi.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'clone="IMAGE:30603233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          program coordinator.
                                                                                                                                                                                                                                                                                                                                                                                                  cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="mRNA"
strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA320878
CA320878.1 GI:24538976
                                                                                                                                                                                                                                                                                                                                                                     Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA320878
                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="whole brain"
/dev stage="embryo 12.5 dpc"
/lab_host="DH108 (TI phage resistant)"
/clone lib="MIH18 MAP FCO"
/clone lib="In H118 MAP FCO"
/clone lib="In H118 MAP FCO"
/clone lib="MIH18 MAP FCO"
/clone lib="MiH18 MAP FCO"
/clone lib="Cording to
/clone lib="Mih18 MAR was size fractionated on a la agarose
/clone lib="Cording to mRNA size fraction,
/clone directionally into pix-Anc vector. The library tag
/clone directionally into pix-Anc vector. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFTZ5482 680 bp mRNA linear EST 09-OCT-2003 UI-M-GZO-cjm-c-18-0-UI.rl NIH_BMAP_GZO Mus musculus cDNA clone IMAGE30603233 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Expending by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                                                                                      This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                          The following repetitive elements were found in this cDNA sequence: 7-103, >PB1D10#SINE/Alu (matched compliment) 45-185, >B4#SINE/B4 (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 680)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 GIGCTIGGGAAGCAAGCGCICTACCAACIGAGCIACACCCTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30.8; DB Pred. No. 0.37; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:6401543"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:37599650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷. .665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF725482.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
CF725482
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURES
          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
```

ઠે 셤 

```
/tissue type="whole eye"
/dev stage="whole eye"
/dev stage="whole eye"
/dev stage="whole eye"
/dev stage="whole or in phage resistant)"
/clone lib="NIH BMAP GZO"
/clone lib="NIH BMAP GZO"
/note="Organ: Bye; Vector: pXX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed accordings
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel:First strand cDNA synthesis was primed with Oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAGT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

Estiurognathi; Muroidea; Muridae; Murinae; Mus.

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

Sciurognathi; Muroidea; Muridae; Mus.

Sciurognathi; Muroidea; Muridae; Mus.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim.Lin, University of Iowa cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA320878 11near EST 09-JUL-2003
UI-M-FWO-ccb-f-24-0-UI.rl NIH BMAP_FWO Mus musculus cDNA clone
IMAGE:6817273 5', mRNA sequence.
                                                                                                                                         sequence: 1-116, SURRIB#DNA/MER1 type 300-442, >B1 MM#SINE/Alu
(matched compliment) 346-442, >PB1D10#SINE/Alu (matched compliment)
384-524, >B4A#SINE/B4 (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                           The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.3%; Score 30.8; DB 6; Length 680; Best Local Similarity 83.3%; Pred. No. 0.37; Matches 35; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 GIGCITGGGAAGCAAGCGCICTACCAACTGAGCTACACCCIC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
```

```
434-530, >PB1D10#SINE/Alu (matched compliment) 472-612,
>B4A#SINE/B4 (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.3%; Score 30.8; DB 83.3%; Pred. No. 0.37; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Leishmania major"
                                                                                                                                                             'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                        tissue_type="whole eye"
                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:30603899"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             program coordinator.
                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL390545.1 GI:9501521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alicat@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                   Seq primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9477341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                      Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P862R/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                            /organism="musculus"
// fatain="C57BL/6"
// fatain="C57BL/6"
// fatain="C57BL/6"
// fatain="C57BL/6"
// fasue_type="whole brain"
// fow stage="embryo 13:5,14:5,16.5,17.5dpc"
// fow stage="embryo 13:5,14.5,16.5,17.5dpc"
// fow lib_nost="bring"
// for lib_nost="brain; Vector: pyx-Asc; Site_1: EcoR I;
// for lib_nost="brain; Vector: pyx-Asc; Vector: pyx-Asc; Vector: The library tag
// for lib_nost="brain; Vector: pyx-Asc; Vector: The library tag
// for Brain Anatomy Project (BMAP): 'Gene Discovery in the
// for lib_nost="brain; Vector: Byx-Asc; Vector: pyx-Asc; Vecto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E 1 (bases 1 to 729)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Uppublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Distribution information can be found at thtp://genome.uiowa.edu/distribution/Mouseff.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UI-W-GZO-cjr-o-12-0-UI.rl NIH BMAP_GZO Mus musculus cDNA clone CF732823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following repetitive elements were found in this cDNA sequence: 1-33, >PB1D9#SINE/Alu (matched compliment) 43-204, >URR1B#DNA/MER1_type 388-530, >B1_MM#SINE/Alu (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                             The following repetitive elements were found in this cDNA sequence: 26-166, >L1MB4#LINE/L1 (matched compliment) Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.3%; Score 30.8; DB 6; Length 719; 83.3%; Pred. No. 0.37; ive 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GTGCTTGGGAAGCAAGCGCTCTACCAACTGAGCTACACCCTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  program coordinator."
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF732823.1 GI:37629156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.33
Matches 35; Conservative
                                                                                                                                                                                                                                       Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF732823
                                                                                                                                                                                               FEATURES
```

ò

```
/dev stage="wnote eye"
/dev stage="wnote eye"
/lab_host="DH10B (T1 phage resistant)"
/clool_lib="Will BMAP_GZ0"
/note="Organ: Eye; Vector: pXx- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
lows Brain Annatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (24-JUL-2000) Leishmania major Friedlin genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          see http://www.ebi.ac.uk/parasites/leish.html
Details of Leishmania sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/L_major/
at http://www.sanger.ac.uk/Projects/L_major/
The primer sequence can be obtained from alicat@sanger.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 25-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 427)

vens, A.C., Lewis, S.M., Bagherzadeh, A., Zhang, L., Chan, H.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P862R
Leishmania major Friedlin PAC P862 right end-sequence, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taylor, R.G., Huckle, E.E.J., Ivens, A.C., Rajandream, M.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania major
Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A physical map of the Leishmania major Friedlin genome Genome Res. 8 (2), 135-145 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 GTGCTTGGGAAGCAAGCCTCTACCAACTGAGCTACACCCTC 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
```

```
Enkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaleae; Triticeae; Tritice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE430009

503 bp mRNA linear EST 26-JUL-2000
TAS006.B02R990616 ITEC TAS Wheat cDNA Library Triticum aestivum
cDNA clone TAS006.B02, mRNA sequence.
BE430009.1 GI:9427852
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                     71.0%; Score 29.8; DB 11; Length 427; 82.9%; Pred. No. 0.86; 1ive 0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .503
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="TASO06.B02"
/clone_lib="ITEC TAS Wheat cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 ACCTTGGCAAGGTTGCGCTCTACCAACTGAGCTACTCCCGC 282
                                                                                                                                                                                                                                                                                                                                                                                                       2 AGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Gopalan.Selvaraj@nrc.ca
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
/mol_type="genomic DNA"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="PAC P862"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                               Best Local Similarity 82.99
Matches 34; Conservative
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
BE430009/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

ö

Gaps

ö

Query Match 71.0%; Score 29.8; DB 2; Length 503; Best Local Similarity 82.9%; Pred. No. 0.87; Matches 34; Conservative 0; Mismatches 7; Indels

369 Acciriogcaagoiriococrciaccaacitoagciacticcocc 329

8 8

Search completed: January 10, 2006, 19:25:38 Job time : 3798 secs

2 AGCTTGGGAAGCTCGTGCTCTACCAACTGAGCTACCACCGC 42

loiqzu) Anola 9009 zint